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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:54:50 ; Search time 8.35821 Seconds
(without alignments)
102.397 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595
Sequence: 1 AYGIGDITELKRIASMAGR.....SITHTKEYAAAVIERLSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159.5	26.8	125	US-10-467-657-7284	Sequence 7284, Ap
2	69	11.6	653	US-10-821-234-1286	Sequence 1286, Ap
3	65.5	11.0	558	US-10-467-657-694	Sequence 694, App
4	63.5	10.7	141	US-10-467-657-3066	Sequence 3066, Ap
5	63	10.6	567	US-10-793-626-3184	Sequence 3184, Ap
6	63	10.6	805	US-10-927-641-77	Sequence 77, App
7	62.5	10.5	308	US-11-194-246-286	Sequence 286, App
8	62.5	10.5	525	US-10-793-626-1318	Sequence 1318, App
9	62	10.4	2725	US-11-113-424-52	Sequence 52, App
10	61.5	10.3	228	US-10-467-657-2290	Sequence 2290, Ap
11	61.5	10.3	240	US-11-179-977-19	Sequence 19, App
12	61.5	10.3	300	US-10-793-626-1900	Sequence 1900, Ap
13	60	10.1	217	US-11-055-822-316	Sequence 316, App
14	60	10.1	327	US-10-467-657-34	Sequence 34, App
15	60	10.1	341	US-10-467-657-8374	Sequence 8374, Ap
16	60	10.1	691	US-10-467-657-7170	Sequence 7170, Ap
17	59	9.9	450	US-10-995-561-811	Sequence 811, App
18	59	9.9	450	US-10-995-561-815	Sequence 815, App
19	59	9.9	548	US-10-995-561-810	Sequence 810, App
20	59	9.9	567	US-10-995-561-813	Sequence 813, App
21	59	9.9	599	US-10-995-561-812	Sequence 812, App
22	59	9.9	650	US-10-873-528-95	Sequence 95, App
23	59	9.9	724	US-10-821-234-1506	Sequence 1506, App
24	57.5	9.7	196	US-11-065-943-51	Sequence 51, App
25	57.5	9.7	709	US-10-821-234-1138	Sequence 1138, App

26	57	9.6	176	6	US-10-467-657-174	Sequence 174, App
27	57	9.6	176	6	US-10-467-657-3688	Sequence 3688, App
28	57	9.6	437	7	US-11-199-124-2	Sequence 2, App
29	57	9.6	438	7	US-11-199-124-10	Sequence 10, App
30	57	9.6	622	7	US-11-199-124-12	Sequence 12, App
31	56.5	9.5	724	6	US-10-793-626-3082	Sequence 3082, App
32	56	9.4	395	6	US-10-793-626-26	Sequence 26, App
33	56	9.4	635	6	US-10-821-234-1573	Sequence 1573, App
34	56	9.4	908	6	US-10-821-234-1267	Sequence 1267, App
35	56	9.4	964	7	US-11-016-706-39	Sequence 39, App
36	55.5	9.3	312	6	US-10-873-528-69	Sequence 69, App
37	55.5	9.3	419	6	US-10-793-626-2516	Sequence 2516, App
38	55.5	9.3	421	6	US-10-858-730-2	Sequence 2, App
39	55.5	9.3	533	6	US-10-873-528-60	Sequence 60, App
40	55.5	9.3	4384	6	US-10-821-234-1120	Sequence 1120, App
41	55	9.2	410	6	US-10-467-657-2312	Sequence 2312, App
42	55	9.2	1404	6	US-10-878-556A-169	Sequence 169, App
43	54.5	9.2	65	6	US-10-467-657-7342	Sequence 7342, App
44	54.5	9.2	505	6	US-10-793-626-1550	Sequence 1550, App
45	54.5	9.2	730	7	US-11-113-424-50	Sequence 50, App

ALIGNMENTS

```

RESULT 1
US-10-467-657-7284
; Sequence 7284, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: MONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn99, version 1.04
; SEQ ID NO 7284
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7284

Query Match      26.8%; Score 159.5; DB 6; Length 125;
Best Local Similarity 48.8%; Pred. No. 1.3e-10;
Matches 42; Conservative 11; Mismatches 30; Indels 3; Gaps 2;

QY      2 YGIGDITELKRIASMAGR-QKRFARITRSELDQYELSEKRNFLAGFAAKAFA 60
        |||||
DB      3 YGIGDITELKRIASMAGR-QKRFARITRSELDQYELSEKRNFLAGFAAKAFA 60
        |||||

QY      61 KAFGTGIGRQLSPDIEIRKQNGKP 86
        |||||
DB      61 KAVGTGIRGAVSFNCNIGHDALGKP 86
        |||||

RESULT 2
US-10-821-234-1286
; Sequence 1286, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A

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; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc SEQ_genes Version 1.0
; SEQ ID NO 1286
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1286

Query Match          11.6%; Score 69; DB 6; Length 653;
Best Local Similarity 33.8%; Pred. No. 5.1;
Matches 26; Conservative 12; Mismatches 31; Indels 8; Gaps 4;

QY      10 ELKRIAS---MAGROKFAERILTRSELDQY-YELSEK-RKNEFLAGRFAA--KEAFSK 61
      536 EIERMVNDAEKFAEDDKLKERIDTRNELESYAAYSLKNQIGDKELGKLSSEDKETMEK 595
DB      62 AFGTIGRQLSFQDIEI 78
      596 AVEKIEWLESHQDADI 612

RESULT 3
US-10-467-657-694
; Sequence 694, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 694
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-694

Query Match          11.0%; Score 65.5; DB 6; Length 558;
Best Local Similarity 26.6%; Pred. No. 10;
Matches 34; Conservative 29; Mismatches 36; Indels 29; Gaps 9;

QY      5 GIDITELKRIASMAGRO--KRFARILITRSELDQY--LSEKR-----KNIEF--LAGRF 53
      76 GLAV-ENERLATQQLGERKFAFAQYALERQINQVETDSESRQIVRDVQNDLSVGKRF 134
DB      54 AAKEAFSAKFGTIGRQLSF-ODIEIRKQNGKPKYITCKLSQAAVHVSITTKRYAAQ 112
      135 AAAE-----KQIAYLOKEKAEARLRQSH---TELQEKQAQGLAVEN--ERLATQ 178
QY      113 VIERLSS 120
      179 IEQERLAS 186
DB
```

```

; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 3066
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3066

Query Match          10.7%; Score 63.5; DB 6; Length 141;
Best Local Similarity 27.6%; Pred. No. 2.9;
Matches 32; Conservative 22; Mismatches 31; Indels 31; Gaps 8;

QY      18 AGROKRFARILIT-RSELDQYELSEKRN--EFLAGRFAKFAF---SKA-----SKA----- 62
      15 AAQTVWADIVFSCKTDNNKXIEVQKINRLYEYSPSAKKEIAINNSKADLLGRSDRW 74
DB      63 FGTIGRQLSFQDIEIRKQNGK-PYIICTKLSQAAVHVSITTKRYAAQVIER 117
      75 QGMSGRRAIW-----KFQNGEFMYTWIGFD-----SVTITE---SSGVVER 115

RESULT 5
US-10-793-626-3184
; Sequence 3184, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3184
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3184

Query Match          10.6%; Score 63; DB 6; Length 567;
Best Local Similarity 29.9%; Pred. No. 19;
Matches 26; Conservative 15; Mismatches 36; Indels 10; Gaps 4;

QY      2 YGIDITELKRIASMAGROKRFARILITRSELDQYEL-----SEKKNELAGRFAAKE 57
      380 YGDRFRTITQGLMLDGGG-VAQFAEGI-----EVGQVRLGTIKYSNNATFLDNQKQAP 434
DB      58 AFSKAFGTIGRQLSFQDIEIRKQNG 84
      435 LIMGCTIGIVSRILS-AIVEQNNDENG 460
QY
```

```

RESULT 4
US-10-467-657-3066
; Sequence 3066, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
```

```

RESULT 6
US-10-927-641-77
; Sequence 77, Application US/10927641
; Publication No. US20050244966A1
; GENERAL INFORMATION:
; APPLICANT: Pereira, Ranjan
; APPLICANT: Rice, Stephen
```

```

; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; APPLICANT: Wood, Marion
; APPLICANT: Visser, Elizabeth
; TITLE OF INVENTION: Compositions and Methods for the
; FILE OF INVENTION: Modification of Gene Expression
; FILE REFERENCE: 11000.1036C4
; CURRENT APPLICATION NUMBER: US/10/927,641
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/10/137,036
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: PCT/NZ 01/00115
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-927-641-77

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Query Match          10.6%; Score 63; DB 6; Length 805;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 24; Conservative 17; Mismatches 27; Indels 22; Gaps 4;

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QY 2 YGIGDITLTKRIASAGKQKPAERILRLSELDQYELSEKKNFLAGFAKAFK 61
DB 592 YGNSKRLRLANLVVVGSRKRSKOLEOSEKKNYDILEYK--LNGOF----- 640
QY 62 AFGTGIGRQLSPQDIEIRKDKNGKPY-IIC 90
DB 641 -----RWISSQMRVR--NGELYRYIC 660

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RESULT 7
US-11-194-246-286
; Sequence 286, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Molt, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; FILE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (MAR 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 286
; LENGTH: 308
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-286

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Query Match          10.5%; Score 62.5; DB 7; Length 308;
Best Local Similarity 27.1%; Pred. No. 9,9;
Matches 19; Conservative 10; Mismatches 18; Indels 23; Gaps 2;

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QY 38 YELSEKRNELIAGFAKAFKAFK-----TGIGRQLSPQDIEIR 79
DB 126 FKFGSKQ-----GNFAMLOAKSRFGFIVEDNRSFCIDAQRISTTAIRKLANDDQLA 180
QY 80 KDQNGKPYII 89
DB 181 ENLIGKPYRI 190

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RESULT 8
US-10-793-626-1318
; Sequence 1318, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1318
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1318

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```

Query Match          10.5%; Score 62.5; DB 6; Length 525;
Best Local Similarity 26.8%; Pred. No. 19;
Matches 26; Conservative 13; Mismatches 31; Indels 27; Gaps 4;

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QY 19 GKRKFARITITRSRLDQYELSEK-----KNEFLAGFAKAFKAFKGTGIGR 69
DB 49 GRIIRISEKI--GPELRQYFANDNEGKPFPSRSDYKIVLAKYKSR--WISFOTG--- 100
QY 70 QLSFQDIEIRKDKNGKPYIICTKLSQAAVHSITHTK 106
DB 101 -----KDYEGFYIONTMPELQATELHIDHTE 127

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RESULT 9
US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02

```

; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-52

Query Match 10.4%; Score 62; DB 7; Length 2725;
Best Local Similarity 27.4%; Pred. No. 1.7e+02;
Matches 29; Conservative 15; Mismatches 50; Indels 12; Gaps 4;

Qy 12 KRISMAQRO-KRFAERILITRSELDQYVELSEKRNFLAGFAKFAFGTGIQRQ 70
Db 2016 ROTGPLIGRQIFRESEGLVNAKRPDYSY-----NMF-----RVISMQAVINETPLPID-L 2064

Qy 71 LSPQDIEIRKQNGKPYIITCTLSQAAVVSVITHTKEXAAOVVIE 116
Db 2065 YRYVDVSGRTQFGKFSVINYDLNQVITTTVMKHTKIFSANGQVIE 2110

RESULT 10

US-10-467-657-2290
; Sequence 2290, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 2290
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2290

Query Match 10.3%; Score 61.5; DB 6; Length 228;
Best Local Similarity 26.7%; Pred. No. 8.7;
Matches 28; Conservative 8; Mismatches 32; Indels 37; Gaps 5;

Qy 8 ITELKRIS-MAGROKFAERILITRSELDQYVELSEKRNFLAGFAKFAFG-- 64
Db 25 LPEARTACRLIGRLORFVGSV--KQELDTQIELELRK-----VKQAFEXAAOV 73

Qy 65 -----TGIGRQLSPQDI-----EIRKQNGKP 86
Db 74 RDLAKETPTDQNSLHDISDGLKPWEKLEPQRTPADFGVDENGNP 118

RESULT 11

US-11-179-977-19
; Sequence 19, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydroxase-Fold Enzymes
; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 240
; TYPE: PRT

; ORGANISM: Bacillus
US-11-179-977-19

Query Match 10.3%; Score 61.5; DB 7; Length 240;
Best Local Similarity 25.5%; Pred. No. 9.3;
Matches 37; Conservative 14; Mismatches 45; Indels 49; Gaps 7;

Qy 5 GLDITELKRISMAQROKFAERILITRSELDQ-----YVELSEKRNFLAG----- 51
Db 46 GHDFRIGRI-----GRQ-----VEELSKREIDRIIGVPIKDYKERNYTHPESKFSAY 98

Qy 52 -RFAKFAFSKA-----FGTIGRQL-----SFQDIEIRKQNGK 85
Db 99 KRFLAHLEVPADDEPYTQIGYGRTLIGSLGATVSLMTALDYPNFMGNIIMQSPYVDK 158

Qy 86 PYITCTLSQAAVVSVITHTKEXAAOVVIE 107
Db 159 HVLAVKQSDDIKHLSTYHQTGKE 183

RESULT 12

US-10-793-626-1900
; Sequence 1900, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1900
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1900

Query Match 10.3%; Score 61.5; DB 6; Length 300;
Best Local Similarity 20.7%; Pred. No. 12;
Matches 29; Conservative 26; Mismatches 46; Indels 39; Gaps 5;

Qy 4 IGLDITELKRISMAQROK---RFAERILTR-----SELDQYVE 39
Db 76 VGTVAVLTSVAMIPGHEAVVFNFPSRLTLALIGLVAGLVNFIILPPKYYHOLEBOLA 135

Qy 40 LSEK-----RQNEFLAGFAKFAKFAFGTGIQRQ-----LSQDIEIRKQNGKP 86
Db 136 LSEKMYRLFEYRCNELLGLGFSSEKTSKELSKINTIAQKVETIMSYQRBELHYHKNEDN 195

Qy 87 YIICTKLSQAAVH--VSITH 104
Db 196 WKLANRLTRAYNNRLPLISH 215

RESULT 13

US-11-055-822-316
; Sequence 316, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zeidler, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN


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CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 316
LENGTH: 217
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-055-822-316

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Query Match      10.1%; Score 60; DB 7; Length 217;
Best Local Similarity 31.2%; Pred. No. 12;
Matches 30; Conservative 12; Mismatches 28; Indels 26; Gaps 6;

QY 34 LDQYVLS--EK-----RKNEFLAGRAFAKFAFSGFGICRQSLFQDIETKXQ 82
DB 24 LHFHQLHLEKALVAHSVDIRAEFGDARWCAHQHL--QLGRDSD-----PILRGE 75
QY 83 NGKPYIICTLSQAAYVSIHTKEYAAQVIERL 118
DB 76 RGNP-----LWPSVSGSLTHDGRPA--VVAPEL 104

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RESULT 14
US-10-467-657-34
Sequence 34, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIIGNANI Vega
APPLICANT: MONACT Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 34
LENGTH: 327
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-34

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Query Match      10.1%; Score 60; DB 6; Length 327;
Best Local Similarity 24.5%; Pred. No. 20;
Matches 36; Conservative 21; Mismatches 44; Indels 46; Gaps 7;

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QY 12 KRISMAGRQKRPFRILTSSELDQYVLSERKNE-----FLAGRAFAKFAKFAKFACT 65

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DB 17 KRAAKESTRQRAVRACTAVRVNDR--NRLSARSKAKENIARMLSG---AKVSEDEALTTC 72
QY 66 GIGRQLSFQDIEIRKQ-----NGKPYII--CTKLSQAAY 98
DB 73 GIMMRLSLQDMRYACNQLINFAEHIVKQVORLGLYCNTDDPANGESVLFACREASQAV 132
QY 99 HVSITHKEY-----AAQVIERLSS 120
DB 133 Q-----WTKDFNLSPNQRLVLRPLSN 155

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RESULT 15
US-10-467-657-8374
Sequence 8374, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIIGNANI Vega
APPLICANT: MONACT Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 8374
LENGTH: 341
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8374

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Query Match      10.1%; Score 60; DB 6; Length 341;
Best Local Similarity 24.5%; Pred. No. 21;
Matches 36; Conservative 21; Mismatches 44; Indels 46; Gaps 7;

QY 12 KRISMAGRQKRPFRILTSRELDQYVLSERKNE-----FLAGRAFAKFAKFAKFACT 65
DB 31 KRAAKESTRQRAVRACTAVRVNDR--NRLSARSKAKENIARMLSG---AKVSEDEALTTC 86
QY 66 GIGRQLSFQDIEIRKQ-----NGKPYII--CTKLSQAAY 98
DB 87 GIMMRLSLQDMRYACNQLINFAEHIVKQVORLGLYCNTDDPANGESVLFACREASQAV 146
QY 99 HVSITHKEY-----AAQVIERLSS 120
DB 147 Q-----WTKDFNLSPNQRLVLRPLSN 169

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Search completed: December 21, 2005, 14:13:52
Job time : 9.35821 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 21, 2005, 13:49:45 | Search time 133.134 Seconds
(without alignments)
376.608 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595
Sequence: 1 AVGIGDITELKRIASMAGR.....SITHTKEYAAQVIERLSS 120

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595	100.0	120	US-09-770-834-2	Sequence 2, Appl1
2	595	100.0	120	US-10-717-138-2	Sequence 2, Appl1
3	591	99.3	121	US-09-771-383-1	Sequence 1, Appl1
4	591	99.3	121	US-09-771-383-11	Sequence 11, Appl1
5	591	99.3	121	US-09-770-834-12	Sequence 12, Appl1
6	591	99.3	121	US-10-717-138-12	Sequence 12, Appl1
7	304	51.1	119	US-10-282-122A-46229	Sequence 46229, A
8	287	48.2	118	US-10-282-122A-60496	Sequence 60496, A
9	281.5	47.3	124	US-10-724-972A-3855	Sequence 3855, Ap
10	279.5	47.0	117	US-10-282-122A-70857	Sequence 70857, A
11	278.5	46.8	119	US-10-282-122A-71569	Sequence 71569, A
12	278	46.7	119	US-09-771-383-5	Sequence 5, Appl1
13	278	46.7	119	US-09-770-834-6	Sequence 6, Appl1
14	278	46.7	119	US-10-717-138-6	Sequence 6, Appl1
15	277	46.6	119	US-09-815-242-5341	Sequence 5341, Ap
16	277	46.6	119	US-09-815-242-12401	Sequence 12401, A
17	275	46.2	119	US-10-282-122A-44196	Sequence 44196, A
18	275	46.2	119	US-10-857-625-722	Sequence 722, App
19	269	45.2	117	US-10-282-122A-57376	Sequence 57376, A
20	269	45.2	117	US-10-953-901-230	Sequence 230, App
21	269	45.2	117	US-10-953-901-232	Sequence 232, App
22	267	44.9	117	US-09-815-242-10776	Sequence 10776, A
23	262	44.0	126	US-10-282-122A-52394	Sequence 52394, A
24	250	42.0	117	US-10-501-282-72	Sequence 72, Appl1
25	244	41.0	113	US-10-282-122A-74124	Sequence 74124, A
26	243	40.8	120	US-10-282-122A-74124	Sequence 74124, A
27	243	40.8	120	US-10-472-928-3504	Sequence 3504, Ap

28	243	40.8	122	US-09-815-242-13472	Sequence 13472, A
29	243	40.8	122	US-09-815-242-13649	Sequence 13649, A
30	243	40.8	122	US-09-897-645-1	Sequence 1, Appl1
31	243	40.8	157	US-10-617-320-4199	Sequence 4199, Ap
32	237.5	39.9	126	US-10-282-122A-77481	Sequence 77481, A
33	228.5	38.4	119	US-09-769-736-30	Sequence 70, Appl1
34	227	38.2	119	US-10-282-122A-72422	Sequence 72422, A
35	221.5	37.2	124	US-10-282-122A-51630	Sequence 51630, A
36	221	37.1	118	US-10-282-122A-53026	Sequence 53026, A
37	219.5	36.9	126	US-10-282-122A-69189	Sequence 69189, A
38	209.5	35.2	126	US-10-282-122A-53026	Sequence 6, Appl1
39	201.5	33.9	169	US-09-771-383-6	Sequence 6, Appl1
40	201.5	33.9	169	US-09-770-834-7	Sequence 7, Appl1
41	201.5	33.9	169	US-10-717-138-7	Sequence 8, Appl1
42	201	33.8	126	US-09-771-383-8	Sequence 9, Appl1
43	201	33.8	126	US-09-770-834-9	Sequence 9, Appl1
44	201	33.8	126	US-10-717-138-9	Sequence 9, Appl1
45	200.5	33.7	126	US-10-282-122A-78498	Sequence 78498, A

ALIGNMENTS

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RESULT 1
US-09-770-834-2
; Sequence 2, Application US/09770834
; Publication No. US20030211588A1
; GENERAL INFORMATION:
; APPLICANT: Patris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/09/770,834
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-770-834-2
Query Match      100.0%; Score 595; DB 3; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AVGIGDITELKRIASMAGRKRPFRILTRSELDQYELSEKRNKFLAGFAAKEARS 60
Db      1 AVGIGDITELKRIASMAGRKRPFRILTRSELDQYELSEKRNKFLAGFAAKEARS 60
QY      61 KAVGTIGRQLSFODIEIRKDNQKPYIICTKLSQAQVAHVSTHTKEYAAQVIERLSS 120
Db      61 KAVGTIGRQLSFODIEIRKDNQKPYIICTKLSQAQVAHVSTHTKEYAAQVIERLSS 120
RESULT 2
US-10-717-138-2
; Sequence 2, Application US/10717138
; Publication No. US20040078147A1
; GENERAL INFORMATION:
; APPLICANT: Patris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
```

```
APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
FILE REFERENCE: 2368/14
CURRENT APPLICATION NUMBER: US/10/717,138
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US/09/770,834
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 120
TYPE: PRT
ORGANISM: Bacillus subtilis
US-10-717-138-2
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Query Match 100.0%; Score 595; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AVGIGDITELKRIASMAGRORFPAERILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFS 60
DB 1 AVGIGDITELKRIASMAGRORFPAERILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFS 60
QY 61 KAFGTGIGRQLSFODIEIRKDNQKPYIICTKLSQAAPHVSIHTHKEYAAQVIERLSS 120
DB 61 KAFGTGIGRQLSFODIEIRKDNQKPYIICTKLSQAAPHVSIHTHKEYAAQVIERLSS 120
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RESULT 3
US-09-771-383-1

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; Sequence 1, Application US/09771383
; Patent No. US20020094562A1
; GENERAL INFORMATION:
; APPLICANT: Parriss, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
FILE REFERENCE: 2368/12
CURRENT APPLICATION NUMBER: US/09/771,383
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/178,639
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 121
TYPE: PRT
ORGANISM: B. subtilis
US-09-771-383-1
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Query Match 99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 YGIGDITELKRIASMAGRORFPAERILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFS 61
DB 3 YGIGDITELKRIASMAGRORFPAERILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFS 62
QY 62 AFGTIGRQLSFODIEIRKDNQKPYIICTKLSQAAPHVSIHTHKEYAAQVIERLSS 120
DB 63 AFGTIGRQLSFODIEIRKDNQKPYIICTKLSQAAPHVSIHTHKEYAAQVIERLSS 121
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RESULT 4
US-09-771-383-11
; Sequence 11, Application US/09771383

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Patent No. US20020094562A1
GENERAL INFORMATION:
APPLICANT: Parriss, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
FILE REFERENCE: 2368/12
CURRENT APPLICATION NUMBER: US/09/771,383
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/178,639
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11
LENGTH: 121
TYPE: PRT
ORGANISM: Bacillus
US-09-771-383-11
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Query Match 99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 YGIGDITELKRIASMAGRORFPAERILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFS 61
DB 3 YGIGDITELKRIASMAGRORFPAERILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFS 62
QY 62 AFGTIGRQLSFODIEIRKDNQKPYIICTKLSQAAPHVSIHTHKEYAAQVIERLSS 120
DB 63 AFGTIGRQLSFODIEIRKDNQKPYIICTKLSQAAPHVSIHTHKEYAAQVIERLSS 121
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RESULT 5
US-09-770-834-12

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; Sequence 12, Application US/09770834
; Publication No. US20030211588A1
; GENERAL INFORMATION:
; APPLICANT: Parriss, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
FILE REFERENCE: 2368/14
CURRENT APPLICATION NUMBER: US/09/770,834
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 121
TYPE: PRT
ORGANISM: Bacillus sp.
US-09-770-834-12
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Query Match 99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 YGIGDITELKRIASMAGRORFPAERILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFS 61
DB 3 YGIGDITELKRIASMAGRORFPAERILTRSELDQYVELSEKRNKNEFLAGRFAAKEAFS 62
QY 62 AFGTIGRQLSFODIEIRKDNQKPYIICTKLSQAAPHVSIHTHKEYAAQVIERLSS 120
DB 63 AFGTIGRQLSFODIEIRKDNQKPYIICTKLSQAAPHVSIHTHKEYAAQVIERLSS 121
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RESULT 6
US-10-717-138-12
; Sequence 12, Application US/10717138
; Publication No. US20040078147A1
; GENERAL INFORMATION:
; APPLICANT: Parits, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/10/717,138
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/770,834
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-717-138-12

Query Match          99.3%; Score 591; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.8e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 YGIGDITELKRIASMAAGKQKFAERILTRSELDYVEISEKKNIEFLAGRAAKAEAFSK 62
   |||||

QY 62 AGGTGIGRQLSFODIEIRKDNQKPYICTKLSQAAVHSITHTREYAAQVIERLSS 120
   |||||
DB 63 AGGTGIGRQLSFODIEIRKDNQKPYICTKLSQAAVHSITHTREYAAQVIERLSS 121
   |||||

RESULT 7
US-10-282-122A-46229
; Sequence 46229, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
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; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46229
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46229

Query Match          51.1%; Score 304; DB 4; Length 119;
Best Local Similarity 54.2%; Pred. No. 2.3e-28;
Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

QY 3 GIGDITELKRIASMAAGKQKFAERILTRSELDYVEISEKKNIEFLAGRAAKAEAFSK 62
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DB 4 GIGDITELKRIASMAAGKQKFAERILTRSELDYVEISEKKNIEFLAGRAAKAEAFSK 63
   |||||

QY 63 FGTTGIGRQLSFODIEIRKDNQKPYICTKLSQAAVHSITHTREYAAQVIERLSS 120
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DB 64 VGTGIGKVSFLDIEVRNDNRGKPIILITS--TEHIVHSISHSKPEFAVAQVIERLSS 119
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RESULT 8
US-10-282-122A-60496
; Sequence 60496, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
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; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See file wrapper or PAM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 60496
; LENGTH: 118
; TYPE: PRF
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60496

Query Match      48.2%; Score 287; DB 4; Length 118;
Beet Local Similarity 50.9%; Pred. No. 2.5e-26;
Matches 58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 3 GIGLDITELKRIASWAGRQKRFAERILITSSELDQYYEISEKKNEFLAGRAKAENFSKA 62
    |||||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 4 GIGLDMIDERKQVVENKPRFERILTEKEIKQFKYEIGNKIETLAERPAKAEVAA 63

QY 63 FGCTGGRQLSPDIEIRKDQNGEKPYIICTKSQAAVHVSITHTKEYAAAQVIE 116
    |||||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 64 NQTGGKHLSFTDVIELQVEDGRPHVTLPVKSGENVFVSITHTARSAAQVILE 117

RESULT 9
US-10-724-972A-3855
; Sequence 3855, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: PAT#03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO: 3855
; LENGTH: 124
; TYPE: PRF
; ORGANISM: S.epidermidis
US-10-724-972A-3855

Query Match      47.3%; Score 281.5; DB 4; Length 124;
Beet Local Similarity 51.3%; Pred. No. 1.2e-25;
Matches 61; Conservative 20; Mismatches 29; Indels 9; Gaps 4;

QY 2 YGIGDITELKRIASWAGRQKRFAERILT--RSELDQYYEISEKKNEFLAGRAKXA 58
    |||||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 10 YGIGDLIERIKNLQN-QTKFERILITEERDKLNQ--TNEGRLFEFLAGRFVXKA 66

QY 59 ESKAGTGIGRQLSPDIEIRKDQNGEKPYIICTKSQAAVHVSITHTKEYAAAQVIER 117
    |||||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 67 FSKALGTGKGKSVSFODINCYNDAIGKP---CIDPFGYTHVSIHTHTENYAMSQVILEK 122

RESULT 10
US-10-282-122A-70857
; Sequence 7087, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
```

```

; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykand, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 70857
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70857

Query Match      47.0%; Score 279.5; DB 4; Length 117;
Best Local Similarity 51.3%; Pred. No. 2e-25;
Matches 61; Conservative 19; Mismatches 30; Indels 9; Gaps 4;

Qy      2 YGIGADITELKRIISMAGROKRPARIIT--RSELDQYELSEKRNKFLAGRPAKEA 58
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      3 YGIGIDLEIRIKNLQ-NQTKFIRILITIERKLNKY--THQRRLEFLAGRTVEA 59
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy      59 FSKAFGTGIGRQLSPDIEIRKDNKGKPYIICTKLSQAAVHSITHTKEVAAQVIER 117
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      60 FSKALGTGLGKSVSFQDINCYNDAIGKR---CIDYPGFYTHVSITHTENYMSQVILEK 115
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
US-10-282-122A-71569
; Sequence 71569, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykand, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

```

Query Match	46.8%	Score 278.5	DB 4	Length 119
Best Local Similarity	50.0%	Pred No. 2.7e-25		
Matches 59	Conservative 22	Mismatches 32	Indels 5	Gaps 3

RESULT 12
US-09-771-383-5

```

/ GENERAL INFORMATION:
/ APPLICANT: Parits, Kevin
/ APPLICANT: Somers, William
/ APPLICANT: Tam, Amy
/ APPLICANT: Lin, Laura
/ APPLICANT: Stahl, Mark
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
/ TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
/ FILE REFERENCE: 2368/12
/ CURRENT APPLICATION NUMBER: US/09/771,383
/ CURRENT FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: US 60/178,639
/ PRIOR FILING DATE: 2000-01-28
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO: 5
/ LENGTH: 119
/ TYPE: PRT
/ ORGANISM: Staphylococcus
US-09-771-383-5

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Query Match	46.7%	Score 278;	DB 3;	Length 119;
Best Local Similarity	48.7%;	Pred. No. 3.1e-25;		
Matches 57;	Conservative 25;	Mismatches 31;	Indels 4;	Gaps 2.

RESULT 13
US-09-770

; Sequence 6, Application US/09770834
; Publication No. US20030211588A1
; Publication No. US20030211588A1

```

1  APPLICANT: Parris, Kevin
2  APPLICANT: Somers, William
3  APPLICANT: Tam, Amy
4  APPLICANT: Lin, Laura
5  APPLICANT: Stahl, Mark
6  APPLICANT: Powers, Robert
7  APPLICANT: Xu, Guan-Yi
8  TITLE OF INVENTION: CRYSTAL STRUCTURE OF AGPS/ACP COMPLEX, SOLUTION STRUCTURE
9  TITLE OF INVENTION: OF B. SUBSTITIS ACP, AND USES THEREOF
10 FILE REFERENCE: 2368/14
11 CURRENT APPLICATION NUMBER: US/09/770,834
12 CURRENT FILING DATE: 2001-10-12
13 PRIOR APPLICATION NUMBER: US 60/202,466
14 PRIOR FILING DATE: 2000-05-08
15 NUMBER OF SEQ ID NOS: 16
16 SOFTWARE: PatentIn version 3.0
17 SEQ ID NO 6
18 LENGTH: 119
19 TYPE: PR1
20 ORGANISM: Staphylococcus sp.
21 US-09-770-834-6

```

Query Match	46.7%	Score 278;	DB 3;	Length 119;
Best Local Similarity	48.7%;	Pred. No. 3.1e-25;		
Matches 57;	Conservative 25;	Mismatches 31;	Indels 4;	Gaps 2

Oy 2 YGIGDLITELKRIASMGROKRAERILTRSELDQYELS-EKRNEEFLAGRFAAEAFS 60
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 3 HGIQVDLIEIDRIQALYSKPKLVERILTKEQHNNFTHEQRKLEFLAGRFAATKAFFS 62

61 KAFGTGIGRQLSFDIDIEIRKONGKPIICTLSQAHHVSIHTHKEVAQAQVIER 117
OY ||||: ::||: |:||: ||||:|: ||: ||||:|:
63 KALGTGIGKHAFNIDIDCYNDELGKPKI--DYEGLIVHSISHTHEYAMSQVLEK 116
DB

RESULT 14
US-10-717-138-6
; Sequence 6, Application US/10717138
; Publication No. US20040078147A1

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/ APPLICANT: Paris, Kevin
/ APPLICANT: Somers, William
/ APPLICANT: Tam, Amy
/ APPLICANT: Lin, Laura
/ APPLICANT: Stahl, Mark
/ APPLICANT: Powers, Robert
/ APPLICANT: Xu, Guan-Yi
/ TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
/ TITLE OF INVENTION: OF B. SUBSTITIS ACP, AND USES THEREOF
/ FILE REFERENCE: 2368/14
/ CURRENT APPLICATION NUMBER: US/10/717,138
/ CURRENT FILING DATE: 2003-11-19
/ PRIOR APPLICATION NUMBER: US/09/770,834
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 60/202,466
/ PRIOR FILING DATE: 2000-05-08
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 6

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:49 ; Search time 39.403 Seconds
(without alignments)
251.785 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595
Sequence: 1 AYGIGDITELKRIASMAGR.....SITHTKEYAAQVIERLSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfilist.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595	100.0	120	2	US-09-770-834-2
2	591	99.3	121	2	US-09-163-446-4
3	591	99.3	121	2	US-09-770-834-12
4	591	99.3	121	2	US-09-771-383-1
5	591	99.3	121	2	US-09-771-383-11
6	281.5	47.3	124	2	US-09-134-001C-4274
7	278	46.7	119	2	US-09-770-834-6
8	278	46.7	119	2	US-09-771-383-5
9	260	43.7	129	2	US-09-107-532A-6990
10	243	40.8	120	2	US-09-583-110-3157
11	243	40.8	122	2	US-08-987-144-2
12	243	40.8	156	2	US-09-163-446-2
13	243	40.8	157	2	US-09-107-433-4199
14	209.5	35.2	158	2	US-09-543-681A-7596
15	201.5	33.9	159	2	US-09-770-834-7
16	201.5	33.9	169	2	US-09-771-383-6
17	201.5	33.8	126	2	US-09-770-834-9
18	201	33.8	126	2	US-09-771-383-8
19	189.5	31.8	126	2	US-08-728-742A-10
20	189.5	31.8	126	2	US-09-770-834-8
21	189.5	31.8	126	2	US-09-771-383-7
22	189.5	31.8	159	2	US-09-489-039A-11671
23	177.5	29.8	122	2	US-09-198-452A-330
24	177.5	29.8	122	2	US-09-770-834-4
25	177.5	29.8	122	2	US-09-771-383-3
26	177.5	29.8	133	2	US-09-438-185A-315
27	173	29.1	125	2	US-09-770-834-11

28	173	29.1	125	2	US-09-771-383-10	Sequence 10, Appl
29	166.5	28.0	119	2	US-09-770-834-5	Sequence 5, Appl
30	166.5	28.0	119	2	US-09-771-383-4	Sequence 4, Appl
31	152.5	25.6	124	2	US-09-543-681A-6834	Sequence 6834, Ap
32	151	25.4	123	2	US-09-770-834-10	Sequence 10, Appl
33	151	25.4	123	2	US-09-771-383-9	Sequence 9, Appl
34	141.5	23.8	139	2	US-09-770-834-13	Sequence 13, Appl
35	141.5	23.8	139	2	US-09-771-383-12	Sequence 12, Appl
36	134	22.5	126	2	US-09-902-540-10894	Sequence 10894, A
37	129.5	21.8	122	2	US-09-770-834-3	Sequence 3, Appl
38	129.5	21.8	122	2	US-09-771-383-2	Sequence 2, Appl
39	124	20.8	121	2	US-08-728-742A-3	Sequence 3, Appl
40	115	19.3	130	2	US-09-770-834-14	Sequence 14, Appl
41	115	19.3	130	2	US-09-771-383-13	Sequence 13, Appl
42	113	19.0	120	2	US-08-728-742A-1	Sequence 1, Appl
43	107	18.0	376	2	US-09-248-786A-17862	Sequence 17862, A
44	107	18.0	131	2	US-09-602-787A-152	Sequence 15, App
45	101	17.0	122	2	US-08-728-742A-4	Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-09-770-834-2
; Sequence 2, Application US/09770834
; Patent No. 6684162
; GENERAL INFORMATION:
; APPLICANT: Parriss, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/09/770,834
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIORITY FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-770-834-2
;
;
Query Match      100.0%, Score 595, DB 2, Length 120;
Best Local Similarity 100.0%; Pred. No. 8.2e-64;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYGIGDITELKRIASMAGRKPAERITRELDPOYYELSEKRNQFLAGFAAKEAFS 60
DB      1 AYGIGDITELKRIASMAGRKPAERITRELDPOYYELSEKRNQFLAGFAAKEAFS 60
QY      61 KAFGTGIGRQLSFODIEIRKDNQKPYIICITLSSQAAYVHSITHTKEYAAQVIERLSS 120
DB      61 KAFGTGIGRQLSFODIEIRKDNQKPYIICITLSSQAAYVHSITHTKEYAAQVIERLSS 120

RESULT 2
US-09-163-446-4
; Sequence 4, Application US/09163446
; Patent No. 6515119
; GENERAL INFORMATION:
; APPLICANT: Fritz, Christian
; APPLICANT: Youngman, Philip
; APPLICANT: Guzman, Luz-Maria
; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
; FILE REFERENCE: 07334/097001
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;; CURRENT APPLICATION NUMBER: US/09/163,446
;; CURRENT FILING DATE: 1998-09-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 4
;; LENGTH: 121
;; TYPE: PRP
;; ORGANISM: Streptococcus pneumonia
US-09-163-446-4

Query Match 99.3%; Score 591; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2,5e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMAAGROKRPFAERILTRSELDQYELSEKRNKNEFLAGRFAAKEAFSK 61
|||
DB 3 YGIGDITELKRIASMAAGROKRPFAERILTRSELDQYELSEKRNKNEFLAGRFAAKEAFSK 62
|||
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIICTKLSQAAVHVSITHTKEYAAAVVIERLSS 120
|||
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIICTKLSQAAVHVSITHTKEYAAAVVIERLSS 121

RESULT 3
US-09-770-834-12
; Sequence 12, Application US/09770834
; Patent No. 6684162
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/09/770,834
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRP
; ORGANISM: Bacillus sp.
US-09-770-834-12

US-09-770-834-12

Query Match 99.3%; Score 591; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2,5e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMAAGROKRPFAERILTRSELDQYELSEKRNKNEFLAGRFAAKEAFSK 61
|||
DB 3 YGIGDITELKRIASMAAGROKRPFAERILTRSELDQYELSEKRNKNEFLAGRFAAKEAFSK 62
|||
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIICTKLSQAAVHVSITHTKEYAAAVVIERLSS 120
|||
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIICTKLSQAAVHVSITHTKEYAAAVVIERLSS 121

RESULT 4
US-09-771-383-1
; Sequence 1, Application US/09771383
; Patent No. 6957150
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark

;; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
;; TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
;; FILE REFERENCE: 2368/12
;; CURRENT APPLICATION NUMBER: US/09/771,383
;; CURRENT FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: US 60/178,639
;; PRIOR FILING DATE: 2000-01-28
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 121
; TYPE: PRP
; ORGANISM: B. subtilis
US-09-771-383-1

Query Match 99.3%; Score 591; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2,5e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMAAGROKRPFAERILTRSELDQYELSEKRNKNEFLAGRFAAKEAFSK 61
|||
DB 3 YGIGDITELKRIASMAAGROKRPFAERILTRSELDQYELSEKRNKNEFLAGRFAAKEAFSK 62
|||
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIICTKLSQAAVHVSITHTKEYAAAVVIERLSS 120
|||
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIICTKLSQAAVHVSITHTKEYAAAVVIERLSS 121

RESULT 5
US-09-771-383-11
; Sequence 11, Application US/09771383
; Patent No. 6957150
; GENERAL INFORMATION:
; APPLICANT: Parris, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACYL CARRIER PROTEIN SYNTHASE
; TITLE OF INVENTION: AND ACYL CARRIER PROTEIN SYNTHASE COMPLEX
; FILE REFERENCE: 2368/12
; CURRENT APPLICATION NUMBER: US/09/771,383
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/178,639
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRP
; ORGANISM: Bacillus
US-09-771-383-11

Query Match 99.3%; Score 591; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2,5e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMAAGROKRPFAERILTRSELDQYELSEKRNKNEFLAGRFAAKEAFSK 61
|||
DB 3 YGIGDITELKRIASMAAGROKRPFAERILTRSELDQYELSEKRNKNEFLAGRFAAKEAFSK 62
|||
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIICTKLSQAAVHVSITHTKEYAAAVVIERLSS 120
|||
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIICTKLSQAAVHVSITHTKEYAAAVVIERLSS 121

RESULT 6
US-09-134-001C-4274
; Sequence 4274, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

LENGTH: 129 amino acids
TYPE: amino acid

```

?      TOPOLOGY: linear
?      MOLECULE TYPE: Protein
?      HYPOTHETICAL: YES
?      ORIGINAL SOURCE:
?      ORGANISM: Enterococcus faecium
?      FEATURE:
?      NAME/KEY: misc_feature
?      LOCATION: (B) LOCATION 1...129
?      SEQUENCE DESCRIPTION: SEQ ID NO: 6990:
?      US-09-107-532A-6990

```

Query Match	43.7%	Score 260;	DB 2;	Length 129;
Best Local Similarity	48.2%;	Pred. No. 1.8e-23;		
Matches 55;	Conservative 22;	Mismatches 35;	Indels 2;	Gaps 2

```

Qy      3 GIGDLITELKRIASMAGRQKRFARILTRSELDQYELSEKRNKNEFLAGFAKAFSKA 62
      |||:| ||| : : ||| | : : ||| ||| :| ||| |||
Db     17 GIGIDAVELPRITRLIEKKPKFARILTSDEMKLFQSLDPFHROVEFLGGYVACKKAFSKA 76

```

```

QY      63  FGTGIGRQLSFODIEIRKQNGKPYIICTKLQAAVHVSITHTKEYAAQVIE 116
        :||||:||||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      77  WGTGIGK-VTFQDVEIKNENGQD-VVTSHPHGNTAVSITHTNETAFQIILE 128

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RESULT 10
US-09-583-110-3157
; Sequence 3157, Application US/09583110

Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
 FILE REFERENCE: PATH00-07A
 CURRENT APPLICATION NUMBER: US/09/583,110

; PRIOR APPLICATION NUMBER: US 09/107,433
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/085,131

;
 ;
 ; PRIOR APPLICATION NUMBER: US 60/051,553
 ;
 ; PRIOR FILING DATE: 1997-07-02
 ;
 ; NUMBER OF SEQ ID NOS: 5322
 ;

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; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3157

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Query Match	40.8%;	Score 243;	DB 2;	Length 120;
Best Local Similarity	44.1%;	Pred. No. 1.8e-21;		
Matches	52;	Conservative	25;	Mismatches 31;
				Indels 10;
				Gaps 3

Qy 3 GIGDITELKRIASMAQRKRFAIRILTRSELDQYELSEKRNKEFIAGRPAKAERFSA 62
| : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 4 GHGIDIEELASIESAVTHHEGFAPKRVLTQEMERTSLKGRRQEIFIAGRPSAKAEAFSA 63

Dy

63 FGTGIGRQLSPDIEIRKQNGRPYIICTKLSCA----AVHVSITHTREVAQAQVVE 116
||||| : ||||| :: : | | |
 : : ||| : ||| :

Db

64 MGTGISRK-LGFQLEVLNNRGAPY---FSQAPSFGKIWTSISHTDOFVTLSVILE 115

RESULT 11
US-08-987-144-2
; Sequence 2, Application US/08987144

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;
; GENERAL INFORMATION:
;
; APPLICANT:  Rotheck Jr., Paul R.
;
; TITLE OF INVENTION:  Streptococcus Pneumoniae Gene Sequence
;

```

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Eli Lilly and Company
;; STREET: Lilly Corporate Center

```

; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: U.S.
; ZIP: 46285
; COMPUTER READABLE FOR

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```

COMPUTER:  IBM PC compatible
OPERATING SYSTEM:  PC-DOS/MS-DOS
SOFTWARE:  PatentIn Release #1.0, Version #1.30

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APPLICATION NUMBER: US/08/987,144
FILING DATE: December 8, 1997
CLASSIFICATION: 424

NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-

TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

LENGTH: 122 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

MOLECULE 1
US-08-987-144-2

Query Match	40.8%	Score 243	DB 21	Length 122
Best Local Similarity	44.1%	Pred. No. 1.8e-21		
Matches 52	Conservative 25	Mismatches 34	Indels 10	Gaps 3

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Qy      3 GIGDITELKRIASMAGRQKPRAERILTRSELDQYVEISEKRKQEFLAGGPAKAFA SKA 62
          | : ||| | : ||| : ||| : : ||| : ||| : ||| : ||| : ||| : |||
Db      6 GHGIDIEELASIESAVTRHEGGAQRVLTAQEMERFTSLGRQLEYLAGRWSAKAFA SKA 65
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QY      63 FGTGIRQLSPFDIEIRKDQNGKPYIICTKLQA----AVHSITHTKEYAAQVIE 116
        |||| : ||| : : : ||| : ||| : : ||| : : ||| :
Db      66 MGTGISLK-LGFDDLEVLNNRGAPY-----FSQAPPSGKINLISISTDQFVTASVILE 117
```

RESULT 12
US-09-163-446-2

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; GENERAL INFORMATION:
; APPLICANT: Fritz, Christian
; APPLICANT: Youngman, Philip

```

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; TITLE OF INVENTION: USE OF S-YDCB AND B-YDCB, ESSENTIAL BACTERIAL GENES
; FILE REFERENCE: 07334/097001
; CURRENT APPLICATION NUMBER: US/09/163,446

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; NUMBER OF SEQ ID NOS: 12
;
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2

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; ORGANISM: Streptococcus pneumonia
;
US-09-163-446-2

```

Best Local Similarity 44.1%; Pred. No. 2.6e-21;
Matches 52; Conservative 25; Mismatches 31; Indels 10; Gaps 3.

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40 GHGIDIEELASIESAVTRHEGFAKRVLTAQEMERFTSLKGRQIETLGRWSAKEAFSKA 99

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Db 100 MGTGISK-LGFDLEVLNNERGABY-----FSQAPPSGKIMWISISHTDQFVTAIVLE 151

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FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7596
LENGTH: 138
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7596

Query Match          35.2%; Score 209.5; DB 2; Length 138;
Best Local Similarity 41.1%; Pred. No. 2,3e-17;
Matches 51; Conservative 22; Mismatches 40; Indels 11; Gaps 4;

QY      3 GIGLDITELKRIASMAGRQ-KPAERILTRSELDQYYELSEKKNEFLAGFPAKEAFSK 61
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
DB      17 GGMGDIVEISRIEIIIGRGGERLARIRLIDNEMILIYC--SHKOPVRFIAKFVAVEAAAK 74

QY      62 ARGTGIGRGLSFODIEIRKDONGKRYI-----ICTLSQA----AVHSITHTKEXAAAQV 113
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
DB      75 AAGTGTGRLGLAPNFHFEVANDELGGPTLHPFLAVAKEMAKAGINAIHTVLADQRACATV 134

QY      114 VIER 117
        ::||
DB      135 ILEK 138

RESULT 15
US-09-770-834-7
Sequence 7, Application US/09770834
Patent No. 6684162
GENERAL INFORMATION:
APPLICANT: Paris, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Maik
APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
OF B. SUBTILIS ACP, AND USES THEREOF
FILE REFERENCE: 2368/14
CURRENT APPLICATION NUMBER: US/09/770,834
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 169
TYPE: PRT
ORGANISM: Thermotoga sp.
US-09-770-834-7

Query Match          33.9%; Score 201.5; DB 2; Length 169;
Best Local Similarity 42.4%; Pred. No. 2.8e-16;
Matches 50; Conservative 23; Mismatches 30; Indels 15; Gaps 7;

QY      3 GIGDITELKRISAMGRQKPFAERTLTRSELDOYYELSEKKNEFLAGRPAKEAFSA 62
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
DB      4 GGVDIVLEVERV-----DEKFAERILGSEKERLF--LTRKRREFIARFPALKERFFRA 55

QY      63 FGFGIGROLFSODIEIRKDONGKPYIICTKLSQA--AVHSITHTKEXAAAQVI 117
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::||
DB      56 LGGIJGINH-SFTIVER-LESNGRP-VLCXHKDFGFENVAHVSLSDR-FVALLVLEK 109

Search completed: December 21, 2005, 13:55:50
Job time : 40.403 secs
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RT subtile."
RL Nature 390:249-256(1997).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=21463117; PubMed=11489886; DOI=10.1074/jbc.M103556200;
RA Moocle H.D., Flinking R., Marahiel M.A.;
RT "4'-phosphopantetheine transfer in primary and secondary metabolism of
RT Bacillus subtilis."
RL J. Biol. Chem. 276:37289-37298(2001).
RN [4]
RP MUTAGENESIS OF ILE-2, ILE-5 AND GLN-113, AND X-RAY CRYSTALLOGRAPHY
RP (1.5 ANGSTROMS) OF NATIVE PROTEIN AND COMPLEXES WITH COENZYME A AND
RP WITH HOLO-(ACYL CARRIER PROTEIN).
RX Pubmed=10997907; DOI=10.1016/S0969-2126(00)00178-7;
RA Parisis K.D., Lin L., Tam A., Mathew R., Hixon J., Stahl M.,
RA Fritz C.C., Seehra U., Somers W.S.;
RT "Crystal structures of substrate binding to Bacillus subtilis holo-
RT (acyl carrier protein) synthase reveal a novel trimetric arrangement of
RT molecules resulting in three active sites."
RL Structure 8:883-895(2000).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of fatty acid acyl-carrier protein ACP. Also modifies
CC the D-lamyl carrier protein but fails to recognize PCP and acpP,
CC an acyl carrier protein of secondary metabolism.
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. AcpS
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB001488; BA19299.1; -; Genomic DNA.
CC EMBL; Z89106; CAB12269.1; -; Genomic DNA.
CC PIR; H69772; H69772.
CC PDB; 1F80; X-ray; A/B/C-.
CC DR Subtilast; BG12089; acps.
CC DR HAMAP; MF_00101; -; 1.
CC DR InterPro; IPR008278; 4-PPT_transf.
CC DR InterPro; IPR002582; ACPs.
CC DR InterPro; IPR004568; Pantethn_trans.
CC DR Pfam; PF01648; ACPs; 1.
CC DR ProDom; PD004282; ACPs; 1.
CC DR TIGRFAMs; TIGR00516; acps; 1.
CC DR TIGRFAMs; TIGR00556; pantethn_tm; 1.
CC 3D-structure; Complete proteome; Fatty acid biosynthesis;
CC Lipid synthesis; Magnesium; Metal-binding; Transferase.
CC KM METAL 8 8
CC FT METAL 58 58
CC FT MUTAGEN 2 2
CC FT MUTAGEN 5 5
CC FT MUTAGEN 5 5
CC FT MUTAGEN 5 5
CC FT STRAND 113 113
CC FT MUTAGEN 113 113
CC FT STRAND 2 11
CC FT HELIX 12 21
CC FT TURN 23 24
CC FT TURN 23 24
CC FT HELIX 25 29
CC FT HELIX 32 38
CC FT TURN 33 39
CC FT TURN 40 40
CC FT HELIX 43 64
CC FT TURN 43 65
CC FT STRAND 65 65
CC FT TURN 69 69
CC FT TURN 70 71
CC FT STRAND 72 72
CC FT STRAND 74 76
CC FT HELIX 74 76

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FT STRAND 78 81
FT TURN 83 84
FT STRAND 87 91
FT TURN 92 94
FT TURN 95 105
FT STRAND 95 105
FT STRAND 109 117
SQ SEQUENCE 121 AA; 13718 MW; 6C10401DA7116701 CRC64;

Query Match 99.3%; Score 591; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.2e-47;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIAMGROKRFARILITRSELDQYVELSEKRNELAGFAKAEFSK 61
DB 3 YGIGDITELKRIAMGROKRFARILITRSELDQYVELSEKRNELAGFAKAEFSK 62
QY 62 AFGGIGRQLSFQDIEIRKQNGKPYIITCTLSQAAVHVSITTKETPAQAQVIERLS 120
DB 63 AFGGIGRQLSFQDIEIRKQNGKPYIITCTLSQAAVHVSITTKETPAQAQVIERLS 121

RESULT 2
ACPS_GEOKA STANDARD; PRT; 129 AA.
ID ACPS_GEOKA
AC Q513G7;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocustNames=GK0228;
OS Geobacillus kaustophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxId=1462;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=HTA426;
RX Pubmed=15576355; DOI=10.1093/nar/gkh970;
RA Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
RA Matsui S., Uchiyama I.;
RT "Thermoadaptation trait revealed by the genome sequence of
RT thermophilic Geobacillus kaustophilus."
RL Nucleic Acids Res. 32:6292-6303(2004).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. AcpS
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000043; BAD74513.1; -; Genomic DNA.
CC HAMAP; MF_00101; -; 1.
CC DR InterPro; IPR008278; 4-PPT_transf.
CC DR InterPro; IPR002582; ACPs.
CC DR InterPro; IPR004568; Pantethn_trans.
CC DR Pfam; PF01648; ACPs; 1.
CC DR ProDom; PD004282; ACPs; 1.
CC DR TIGRFAMs; TIGR00516; acps; 1.
CC DR TIGRFAMs; TIGR00556; pantethn_tm; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Magnesium; Metal-binding; Transferase.
CC KM METAL 8 8
CC FT METAL 58 58
CC FT SEQUENCE 129 AA; 14213 MW; 302421348F6526C CRC64;

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Query Match 56.2%; Score 334.5; DB 1; Length 129;
 Best Local Similarity 60.3%; Pred. No. 3.5e-23;
 Matches 70; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

3 GIGLIDITELKRIASMGROKFAERILITRSELDQYVELSEKRNKNEFLAGRFAKAFAFKA 62
 4 GIGLIDIVELERIRSLERSKRPERILITPREKAQOGELPPARQAELFLGRFAKAYAKA 63
 63 FGTGIGRQSLFODIIRKQNGKPYIITCKLSQAAMVHSITHTKEVAAQVIERL 118
 64 LGTIGRHLSPDIEIVDEHCKPSIAARDE-ITVHLSHSRDYAAQVIERL 118

RESULT 3

ACPS_BACSK STANDARD; PRT; 117 AA.

AC 05MAY1;
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holol-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holol-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocNames=ABC0805;
 OS Bacillus clausii (strain KSM-K16)
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=66692;
 [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Takaki Y., Kageyama Y., Shimamura S., Suuki H., Nishi S., Hatada Y.,
 RA Kawai S., Ito S., Horikoshi K.
 RT "The complete genome sequence of the alkaliphilic Bacillus clausii
 KSM-K16."
 RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; AP006627; BAD63344.1; -; Genomic_DNA.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantech_n_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantech_n_tm; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KM Magnesium; Metal-binding; Transferase.
 FT METAL 8 Magnesium (By similarity).
 FT METAL 58 Magnesium (By similarity).
 SQ SEQUENCE 117 AA; 12841 MW; 9389775ED4411A38 CRC64;

Query Match 55.4%; Score 329.5; DB 1; Length 117;
 Best Local Similarity 61.4%; Pred. No. 9.1e-23;
 Matches 70; Conservative 15; Mismatches 28; Indels 1; Gaps 1;

3 GIGLIDITELKRIASMGROKFAERILITRSELDQYVELSEKRNKNEFLAGRFAKAFAFKA 62
 4 GIGLIDITELKRIEAFARQPRFORVLTSEYQDQMAOLAPNRQIEYLAGRFAKAFAFKA 63
 63 FGTGIGRQSLFODIIRKQNGKPYIITCKLSQAAMVHSITHTKEVAAQVIERL 116

DB 64 KGTGIGAGLSWHDIEIRTEGSGKPYIVND-DSARVHLSTHSKEVAAQVIERL 116

RESULT 4

ACPS_BACCR STANDARD; PRT; 119 AA.

AC 08MAY1;
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holol-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holol-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocNames=BC0262;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NCBI_TaxID=226900;
 [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galloway N., Candelon B.,
 RA Kapetral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goldstein E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis."
 RL Nature 423:87-91(2003).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; AE016998; AAP07331.1; -; Genomic_DNA.
 DR HSP; P96618; I77L.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004568; Pantech_n_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantech_n_tm; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KM Magnesium; Metal-binding; Transferase.
 FT METAL 8 Magnesium (By similarity).
 FT METAL 58 Magnesium (By similarity).
 SQ SEQUENCE 119 AA; 13296 MW; 799459B3082D626B CRC64;

Query Match 52.6%; Score 313; DB 1; Length 119;
 Best Local Similarity 54.7%; Pred. No. 3.2e-21;
 Matches 64; Conservative 22; Mismatches 29; Indels 2; Gaps 1;

3 GIGLIDITELKRIASMGROKFAERILITRSELDQYVELSEKRNKNEFLAGRFAKAFAFKA 62
 4 GIGLIDITELKRIEAKLQKMERILITENENVMELKGSRLTFVAGRFAKAFAFKA 63
 63 FGTGIGRQSLFODIIRKQNGKPYIITCKLSQAAMVHSITHTKEVAAQVIERL 119
 64 VGTGIGKEVSLDIEVKDERGKPYIITLTS-TEYIVHLSHSKFAVAAQVIERL 118

RESULT 5

ACPS_BACAN STANDARD; PRT; 119 AA.
 ID ACPS_BACAN 0813G3; 0614F9; 06K1G1;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocustNames=BA0250, GBA0250, BAS0253;
 OS Bacillus anthracis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=1392;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ames / Isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Bailly L.W., Paulsen I.T.,
 RA Nelson K.E., Tettein H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
 RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RA "The genome sequence of Bacillus anthracis Ames and comparison to
 RT closely related bacteria."
 RL Nature 423:81-86(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ames / Isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RA "Bacillus anthracis comparative genomics."
 RT Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Stemne;
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RA "Complete genome sequence of Bacillus anthracis Stemne."
 RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 CC family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AE017024; AAP24289.1; -; Genomic_DNA.
 CC EMBL; AE017334; AAT29331.1; -; Genomic_DNA.
 CC EMBL; AE017225; AAT52572.1; -; Genomic_DNA.
 CC HSSP; P96618; 1F7L.
 CC TIGR; BA0250; -.
 CC TIGR; GBA0250; -.
 CC HAMAP; MF_00101; -; 1.
 CC InterPro; IPR008278; 4-PPT_transf.
 CC InterPro; IPR002582; ACPS.
 CC InterPro; IPR004568; Pantethn_trans.
 CC Pfam; PF01648; ACPS; 1.

DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantethn tm; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferase.
 FT METAL 8 8 Magnesium (By similarity).
 FT METAL 58 58 Magnesium (By similarity).
 SQ SEQUENCE 119 AA; 13100 MM; 8680A0B258813E14 CRC64;
 Query Match 51.1%; Score 304; DB 1; Length 119;
 Best Local Similarity 54.2%; Pred. No. 2.2e-20;
 Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;
 QY 3 GIGDITELKRIASMAKROKFAFIRILTRSLDQYELSEKSKKPLAGRAFAKAFSA 62
 DB 4 GIGDITELNRIEKLGLGKLFMRILITENRNVAKLKSRLTETFAAGRAKAYATSKA 63
 QY 63 FGTSIGRQLSFQDIEIRKDONKGPYIITKLSQAAVHSVITHTKYAAQVITRLSS 120
 DB 64 VGTGIGKEVSFLDIEVRNDRGKRLITS--TEHIVHLISHSKRFPAVAVLESSSS 119
 RESULT 6
 ACPS_BACHK STANDARD; PRT; 119 AA.
 ID ACPS_BACHK 06HBE3;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
 DE (4'-phosphopantetheinyl transferase acps).
 GN Name=acps; OrderedLocustNames=BT9727_0222;
 OS Bacillus thuringiensis (subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OC NCBI_TaxID=180856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=97-27;
 RA Bretlin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RA "Complete genome sequence of Bacillus thuringiensis 97-27."
 RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 CC A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
 CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 CC family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AE017355; AAT62521.1; -; Genomic_DNA.
 CC HAMAP; MF_00101; -; 1.
 CC InterPro; IPR008278; 4-PPT_transf.
 CC InterPro; IPR002582; ACPS.
 CC InterPro; IPR004568; Pantethn_trans.
 CC Pfam; PF01648; ACPS; 1.
 CC ProDom; PD004282; ACPS; 1.
 CC TIGRFAMs; TIGR00516; acps; 1.
 CC TIGRFAMs; TIGR00556; pantethn tm; 1.
 CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferase.
 FT METAL 8 8 Magnesium (By similarity).
 FT METAL 58 58 Magnesium (By similarity).
 SQ SEQUENCE 119 AA; 13100 MM; 8680A0B258813E14 CRC64;

Query Match 51.1%; Score 304; DB 1; Length 119;
 Best Local Similarity 54.2%; Pred. No. 2.2e-20;
 Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

Db 4 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKFLGKFAKFAKFA 62
 63 FTGTGIGRQLSPDIEIRKQNGKPYIICTKLSQAQVHVSITHTKEVAAQVIERLS 120
 64 VGTGIGKEVSLDIEVRNDRGKPIILITS--TEHIVHLSHSKFAVAAQVLESSS 119

RESULT 7
 ACPS_BACCI STANDARD; PRT; 119 AA.
 ID ACPS_BACCI
 AC Q73ET8;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-(acyl-carrier-protein) synthase (EC 2.7.8.7) (Holo-ACP synthase)
 GN Name=acps; OrderedLocustNames=BC0270;
 OS Bacillus cereus (strain ATCC 10987);
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 NCBI_TaxID=222523;
 [1]
 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
 RA Nelson W.C., Kolseoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
 adaptations and a large plasmid related to Bacillus anthracis pXO1."
 RL Nucleic Acids Res. 32:977-988(2004).
 CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
 A to a Ser of acyl-carrier protein (By similarity).
 CC -1- CATALYTIC ACTIVITY: CoA + apo-(acyl-carrier protein) = adenosine
 3',5'-bisphosphate + holo-(acyl-carrier protein).
 CC -1- COFACTOR: Magnesium (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
 family.

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 DR EMBL; AE017264; MAS39206.1; -; Genomic_DNA.
 DR TIGR; BCE0270; -;
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR005282; ACPS_
 DR InterPro; IPR004568; Pantech_n_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; pantech_n; 1.
 KM Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KM Magnesium; Metal-binding; Transferase.
 FT METAL 8 Magnesium (By similarity).
 FT METAL 8 Magnesium (By similarity).
 FT SEQUENCE 119 AA; 13142 MW; 4AAA4DEF92815CDC CRC64;

Db 4 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKFLGKFAKFAKFA 63
 63 FTGTGIGRQLSPDIEIRKQNGKPYIICTKLSQAQVHVSITHTKEVAAQVIERLS 119
 64 VGTGIGKEVSLDIEVRNDRGKPIILITS--TEHIVHLSHSKFAVAAQVLESSS 118

RESULT 8
 Q4MPT7_BACCE PRELIMINARY; PRT; 119 AA.
 ID Q4MPT7_BACCE
 AC Q4MPT7;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Holo-(acyl-carrier-protein) synthase (EC 2.7.8.7).
 GN Name=acps; ORFNames=BC_G9241_0240;
 OS Bacillus cereus G9241.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 NCBI_TaxID=269801;
 [1]
 NUCLEOTIDE SEQUENCE.
 RA Straub G.241;
 RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
 RA Hoffmeyer A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
 RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
 RA Malden M.C.J., Priest F.G., Barker W., Jiang L., Cer R.Z.,
 RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
 RA Popovic T., Fraser C.M.;
 RT "Identification of anthrax toxin genes in a Bacillus cereus associated
 RT with an illness resembling inhalation anthrax";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAEK0100017; EAL14228.1; -; Genomic_DNA.
 KM Transferase.
 SQ SEQUENCE 119 AA; 13142 MW; 0B16DAB5812BDB CRC64;

Query Match 50.9%; Score 303; DB 2; Length 119;
 Best Local Similarity 54.7%; Pred. No. 2.7e-20;
 Matches 64; Conservative 19; Mismatches 32; Indels 2; Gaps 1;

Db 3 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKFLGKFAKFAKFA 62
 4 GIGDITELKRIASMAAGROKFAERILTRSELDQYVEISEKRNKFLGKFAKFAKFA 63
 63 FTGTGIGRQLSPDIEIRKQNGKPYIICTKLSQAQVHVSITHTKEVAAQVIERLS 119
 64 VGTGIGKEVSLDIEVRNDRGKPIILITS--TEHIVHLSHSKFAVAAQVLESSS 118

RESULT 9
 ACPS_BACCC STANDARD; PRT; 119 AA.
 ID ACPS_BACCC
 AC Q63GX2;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Holo-(acyl-carrier-protein) synthase (EC 2.7.8.7) (Holo-ACP synthase)
 GN Name=acps; OrderedLocustNames=BCZK0224;
 OS Bacillus cereus (strain ZK).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 CC Bacillus cereus group.
 NCBI_TaxID=286681;
 [1]
 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus cereus ZK.";

```
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a set of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
-----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC EMBL, CP000001; AAU20010.1; -; Genomic_DNA.
DR HAMAP; MF_00101; -; 1.
DR InterPro; IPR008278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantechm_trans.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantechm_tm; 1.
DR Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KM Magnesium; Metal-binding; Transferase.
FT METAL 8 Magnesium (By similarity).
FT METAL 58 Magnesium (By similarity).
SQ SEQUENCE 119 AA; 13169 MW; 8730A0B258813E14 CRC64;

Query Match 50.4%; Score 300; DB 1; Length 119;
Best Local Similarity 53.8%; Pred. No. 5.1e-20; Indels 2; Gaps 1;
Matches 63; Conservative 20; Mismatches 32;

QY 3 GIGLDITELKRIASMAGROKFAERILTRSELDQYVEISEKRNKEFLAGFAAKEAFSKA 62
DB 4 GTGIDIVELRIEQMLDGKLMERILTENERNVAKGLKGSULTFVAGRAFAAKEAFSKA 63

QY 63 FGTGIGRQLSFODIEIRKQNGKPYIICTKLSQAANVSTHTTKXYAAQVIRLSS 119
DB 64 VGTGIGKEVVSFLDIEVRNDRGKPIILITS--TEHIVHLSHSHSKERAVNAQVIRLSS 118

RESULT 10
ACPS_BACBD STANDARD; PRT; 119 AA.
AC Q9KFG1;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocustNames=BH0518;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=8665;

RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA STRAIN=C-125 / JCM 9153;
RC MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kohara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a set of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
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-----
CC EMBL, BA000004; BAB04237.1; -; Genomic_DNA.
DR PIR; F83714; F83714.
DR HSSP; Q9FTT5; 1PTH.
DR HAMAP; MF_00101; -; 1.
DR InterPro; IPR008278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR004568; Pantechm_trans.
DR Pfam; PF01648; ACPS; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00516; acps; 1.
DR TIGRFAMs; TIGR00556; pantechm_tm; 1.
DR Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KM Magnesium; Metal-binding; Transferase.
FT METAL 8 Magnesium (By similarity).
FT METAL 58 Magnesium (By similarity).
SQ SEQUENCE 119 AA; 13421 MW; 2279E552549041C9 CRC64;

Query Match 49.9%; Score 297; DB 1; Length 119;
Best Local Similarity 50.0%; Pred. No. 9.6e-20; Indels 2; Gaps 2;
Matches 59; Conservative 25; Mismatches 32;

QY 3 GIGLDITELKRIASMAGROKFAERILTRSELDQYVEISEKRNKEFLAGFAAKEAFSKA 62
DB 4 GTGIDIVELRIEQMLDGKLMERILTENERNVAKGLKGSULTFVAGRAFAAKEAFSKA 63

QY 63 FGTGIGRQLSFODIEIRKQNGKPYIICTKLSQAANVSTHTTKXYAAQVIRLSS 120
DB 64 VGTGISAEGVHWDVLSDERGKP-VLSVNL-DATIHVSISHSOSYAIAQVIRLSS 119

RESULT 11
ACPS_LISMF STANDARD; PRT; 118 AA.
AC Q721T0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocustNames=LM02365_0904;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_Taxid=265669;

RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Raeko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Beaman M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forreger H.A., Tran B., Kathariou S., Wondolting L.D., Whittich G.A.,
RA Bayles D.O., Luchaneky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT borne pathogen Listeria monocytogenes reveal new insights into the
RT core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a set of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
```

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CC family.
CC -----
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CC -----
CC EMBL; AE017325; AAT03684.1; -; Genomic_DNA.
CC TIGR; LMOF2365.0904; -.
CC HAMAP; MF_00101; -; 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPS.
CC InterPro; IPR004568; Panethn_trans.
CC Pfam; PF01648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRPFAM; TIGR00516; acps; 1.
CC TIGRPFAM; TIGR00556; panethn_tm; 1.
CC Complete proteome; fatty acid biosynthesis; lipid synthesis;
CC Magnesium; Metal-binding; Transferase.
CC METAL 8 8 Magnesium (By similarity).
CC FT METAL 58 58 Magnesium (By similarity).
CC SQ SEQUENCE 118 AA; 13257 MW; 5584C5C769181B3F CRC64;

Query Match 48.2%; Score 287; DB 1; Length 118;
Best Local Similarity 50.9%; Pred. No. 8.1e-19;
Matches 58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 3 GIGLITTELKRIASMGROKRFARILITRSELDQYVEISEKKNEFLAGFAKFAKSA 62
DB 4 GIGLMDIERKQVQVEKXPRFIERVLTKEIKQFEKYEGRKRIEFLAGFAKFAKSA 63
DB 64 NGTGFGKHSFTFVEILQVEDGRPHVTLPVKSGENVFSITHTAASAAQVIE 117

RESULT 12
ACPS LISMO STANDARD; PRT; 118 AA.
AC 08yAL2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocNames=lm00885;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BGD-e / Serovar 1/2a;
RA MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Rusknock C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
RA Eutian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng B., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT Comparative genomics of Listeria species.;
RL Science 294:849-852(2001).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC 3',5'-bisphosphate + holo-[acyl-carrier protein].
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
```

```
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
CC -----
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CC -----
CC EMBL; AL159197; CAC98963.1; -; Genomic_DNA.
CC PIR; A81185; A81185.
CC DR HSSP; P96618; 1F7L.
CC DR Listerist; LMO00885; -.
CC HAMAP; MF_00101; -; 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPS.
CC InterPro; IPR004568; Panethn_trans.
CC Pfam; PF01648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRPFAM; TIGR00516; acps; 1.
CC TIGRPFAM; TIGR00556; panethn_tm; 1.
CC Complete proteome; fatty acid biosynthesis; lipid synthesis;
CC Magnesium; Metal-binding; Transferase.
CC METAL 8 8 Magnesium (By similarity).
CC FT METAL 58 58 Magnesium (By similarity).
CC SQ SEQUENCE 118 AA; 13257 MW; 5584C5C769181B3F CRC64;

Query Match 48.2%; Score 287; DB 1; Length 118;
Best Local Similarity 50.9%; Pred. No. 8.1e-19;
Matches 58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 3 GIGLITTELKRIASMGROKRFARILITRSELDQYVEISEKKNEFLAGFAKFAKSA 62
DB 4 GIGLMDIERKQVQVEKXPRFIERVLTKEIKQFEKYEGRKRIEFLAGFAKFAKSA 63
DB 64 NGTGFGKHSFTFVEILQVEDGRPHVTLPVKSGENVFSITHTAASAAQVIE 117

RESULT 13
ACPS LISIN STANDARD; PRT; 118 AA.
AC 092DD0;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocNames=lm00884;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CLIP 11262 / Serovar 6a;
RA MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Rusknock C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Cherouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
RA Eutian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng B., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT Comparative genomics of Listeria species.;
RL Science 294:849-852(2001).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
```

```
CC 3',5'-bisphosphate + holo-[acyl-carrier protein]).
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; AL596166; CAC96116.1; -, Genomic_DNA.
CC PIR; AD1543; AD1543.
CC HSSP; P96618; 1P7L.
CC Liscilist; LIND00884; -.
CC HAMAP; MF_00101; -, 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPS.
CC InterPro; IPR004568; Pantech_n_trans.
CC Pfam; PF01648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRPFAMS; TIGR00516; acps; 1.
CC TIGRPFAMS; TIGR00556; pantech_n_tm; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Magnesium; Metal-binding; Transferase.
CC METAL 8 Magnesium (By similarity).
CC METAL 8 Magnesium (By similarity).
CC FT METAL 8 Magnesium (By similarity).
CC SQ SEQUENCE 118 AA; 13281 MW; BFC89CF84BCB985 CRC64;

Query Match
Best Local Similarity 51.3%; Score 283; DB 1; Length 118;
Matches 59; Conservative 17; Mismatches 39; Indels 0; Gaps 0;

QY 3 GIGDITELKRIASMGQRQKPAERILTLRSELDQYELSEKRNKNEFLAGRFAAKEAFSKA 62
DB 4 GIGLMDIDRVAQAVKAPRIFERILTEKETKQYKEGSRKIEFLAGRFAAKEAVYKA 63

QY 63 FETGIGROLSFODIERKQNGKPYIICTKLSQAAVHVSITTHKEVYAAQVIER 117
DB 64 NGTGFGLHSFTDVELQVDERPHVTMPDIKQGETFVSIHTPARSAAQVILIQ 118

RESULT 14
ACPS_STABQ STANDARD; PRT; 117 AA.
ID ACPS_STABQ STANDARD; PRT; 117 AA.
AC Q5CHME4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocustNames=SEI675;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 12228;
RX MEDLINE=2832016; PubMed=12950922;
RX DOI=10.1046/j.1365-2958.2003.03671.x;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Zhao Y.-G., Wang W.-Y., Danchin A., Wen Y.-M.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.,
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).",
RL Mol. Microbiol. 49:157-1593 (2003).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
```

```
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; AE016749; AA005274.1; -, Genomic_DNA.
CC HSSP; P96618; 1P7L.
CC HAMAP; MF_00101; -, 1.
CC InterPro; IPR008278; 4-PPT_transf.
CC InterPro; IPR002582; ACPS.
CC InterPro; IPR004568; Pantech_n_trans.
CC Pfam; PF01648; ACPS; 1.
CC ProDom; PD004282; ACPS; 1.
CC TIGRPFAMS; TIGR00516; acps; 1.
CC TIGRPFAMS; TIGR00556; pantech_n_tm; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Magnesium; Metal-binding; Transferase.
CC METAL 8 Magnesium (By similarity).
CC METAL 8 Magnesium (By similarity).
CC FT METAL 8 Magnesium (By similarity).
CC SQ SEQUENCE 117 AA; 13535 MW; 515246BC1C4DEDC9 CRC64;

Query Match
Best Local Similarity 47.0%; Score 279.5; DB 1; Length 117;
Matches 61; Conservative 19; Mismatches 30; Indels 9; Gaps 4;

QY 2 YGIGDITELKRIASMGQRQKPAERILTLRSELDQYELSEKRNKNEFLAGRFAAKEA 58
DB 3 YGIGDITELRIKRLQ-NQTKFIERILTEERDKLNY--THQRRLFLAGRFTVKEA 59

QY 59 FSKAPGICIGROLSFODIERKQNGKPYIICTKLSQAAVHVSITTHKEVYAAQVIER 117
DB 60 FSKALGTGLGKVSFQDINCYNALGKP--CIDYPGFYTHVSTHTENTAMSOVILIK 115

RESULT 15
ACPS_STABQ STANDARD; PRT; 117 AA.
ID ACPS_STABQ STANDARD; PRT; 117 AA.
AC Q5HME4;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7) (Holo-ACP synthase)
DE (4'-phosphopantetheinyl transferase acps).
GN Name=acps; OrderedLocustNames=SERP1684;
OS Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=176279;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Uitterlbeck T.R., Lee C.,
RA Dimetrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.",
RL J. Bacteriol. 187:2426-2438 (2005).
CC -1- FUNCTION: Transfers the 4'-phosphopantetheine moiety from coenzyme
CC A to a Ser of acyl-carrier protein (By similarity).
CC -1- CATALYTIC ACTIVITY: CoA + apo-[acyl-carrier protein] = adenosine
CC -1- COFACTOR: Magnesium (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the P-Pant transferase superfamily. Acps
CC family.
```

CC -----
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 CC removed.

CC -----
 DR EMBL; CP000029; AAM55047.1; -; Genomic_DNA.
 DR TIGR; SERP1684; -.
 DR HAMAP; MF_00101; -; 1.
 DR InterPro; IPR008278; 4-PPT_transf.
 DR InterPro; IPR002582; ACPS.
 DR InterPro; IPR004368; Panethin_trans.
 DR Pfam; PF01648; ACPS; 1.
 DR ProDom; PD004282; ACPS; 1.
 DR TIGRFAMs; TIGR00516; acps; 1.
 DR TIGRFAMs; TIGR00556; panethin_tm; 1.
 KW Complete proteome; Fatty acid_biosynthesis; Lipid synthesis;
 KW Magnesium; Metal-binding; Transferase.
 FT METAL 8 8 Magnesium (By similarity).
 FT METAL 58 58 Magnesium (By similarity).
 SQ SEQUENCE 117 AA; 13535 MW; 515246BC1C4EDC9 CRC64;

Query Match 47.0%; Score 279.5; DB 1; Length 117;
 Best Local Similarity 51.3%; Pred. No. 4e-18;
 Matches 61; Conservative 19; Mismatches 30; Indels 9; Gaps 4;

QY 2 YGIGLITELKRIASMAAGROKRPAREILT---RSELDQYYELSEKRNKNEFLAGRFAPAKEA 58
 DB 3 YGIGLITELKRIKLNQ-NQTKFIERILITEERDKLNQY--THEQRLEFLAGRFVKEA 59
 QY 59 FSKAFGTGIGRQLSPQDIEIRKDQNGKPYIICTKLSQAAVHSITHTKEYAAQVIER 117
 DB 60 FSKALGTGIGKSVSPQDINCYNDAIGKP--CIDYPGFYTHVSIHTENYAMSQVILEK 115

Search completed: December 21, 2005, 13:54:39
 Job time : 175.925 secs

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This page blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:44 ; Search time 15.5224 Seconds
(without alignments)
743.830 Million cell updates/sec

Title: US-10-717-138-2

Perfect score: 595

Sequence: 1 AYGGIDITTEKRIASMAGR.....SITHTKEYAAQVIERLSS 120

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	591	99.3	121	1	H69772	holo-[acyl]-carrier
2	297	49.9	119	2	F83714	holo-[acyl]-carrier
3	287	48.2	118	2	AE1185	holo-acyl-carrier
4	283	47.6	118	2	AD1543	holo-acyl-carrier
5	275	46.2	119	2	E89999	holo-ACP synthase
6	261	43.9	119	2	C86730	acyl-carrier prote
7	243	40.8	120	2	H95197	holo-[acyl]-carrier
8	243	40.8	120	2	D98064	holo-[acyl]-carrier
9	237.5	39.9	126	2	F82072	holo-[acyl]-carrier
10	221.5	37.2	124	2	B96960	holo-acyl-carrier
11	201.5	33.9	126	2	B72345	holo-[acyl]-carrier
12	201	33.8	126	2	F71662	holo-[acyl]-carrier
13	200.5	33.7	126	2	AF0356	holo-[acyl]-carrier
14	195.5	32.9	126	2	E91057	hypothetical prote
15	192.5	32.4	126	2	B85902	hypothetical prote
16	192.5	32.4	126	2	AG0828	holo-[acyl]-carrier
17	189.5	31.8	126	1	B42294	holo-[acyl]-carrier
18	189	31.8	131	2	A97810	hypothetical prote
19	188.5	31.7	126	2	F84959	holo-[acyl]-carrier
20	180.5	30.3	119	2	C71556	holo-[acyl]-carrier
21	178.5	30.0	125	2	D81833	holo-[acyl]-carrier
22	177.5	29.8	122	2	A86530	acyl-carrier prote
23	177.5	29.8	122	2	B72093	acyl-carrier prote
24	173.5	29.2	125	2	D81710	holo-[acyl]-carrier
25	173	29.1	125	2	F71276	holo-[acyl]-carrier
26	168.5	28.3	125	2	F81197	holo-[acyl]-carrier
27	166.5	28.0	119	1	H64620	holo-[acyl]-carrier
28	162.5	27.3	191	2	AC3413	holo-[acyl]-carrier
29	161.5	27.1	119	2	G71894	holo-[acyl]-carrier

30	158.5	26.6	134	2	H97485	holo-acyl-carrier
31	158.5	26.6	134	2	AH2703	holo-[acyl]-carrier
32	151	25.4	123	2	T35573	probable holo-acyl
33	139.5	23.4	133	2	B87442	holo-[acyl]-carrier
34	134.5	22.6	122	2	G85649	probable acyl-carrier
35	134.5	22.6	122	2	D90789	probable holo-acyl
36	133	22.3	133	2	F75544	holo-acyl-carrier
37	132.5	22.4	124	2	B70101	holo-acyl-carrier
38	132	22.2	115	2	A81286	probable holo-acyl
39	129.5	21.8	122	2	H70370	holo-[acyl]-carrier
40	127.5	21.4	115	2	G82895	holo-acyl-carrier
41	124	20.8	1857	1	S01787	fatty-acid synthas
42	115	19.3	130	2	B87058	holo-[acyl]-carrier
43	115	19.3	130	2	H70870	holo-[acyl]-carrier
44	113	19.0	1885	1	JC4086	fatty-acid synthas
45	104	17.5	119	1	S73864	hypothetical prote

ALIGNMENTS

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RESULT 1
H69772 holo-[acyl]-carrier-protein] synthase (EC 2.7.8.7) - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: H69772
R:Kunze, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berber
C.; Bron, S.; Brownell, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eyrington, J.; Fabret, C.; Ferrati, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Galler
A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F.
A.; Koeber, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A.; Schleich, S.; Schroefer, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
A.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: H69772
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-121 <KUN>
A:Cross-references: UNIPROT:P96618; UNIPARC:UP1000005FF70; GB:Z99106; GB:AL009126; NID:1.
A:Experimental source: strain 168
C:Genetics:
A:Gene: ydcB
C:Superfamily: holo-ACP synthase
C:Keywords: coenzyme A; transferase

Query Match 99.3%; Score 591; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. 4.8e-52;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 YGIGDITTEKRIASMAGRKFAERILTRSEIDQYELSEKRNKEFLAGRFAKAFSK 61
DB 3 YGIGDITTEKRIASMAGRKFAERILTRSEIDQYELSEKRNKEFLAGRFAKAFSK 62
OY 62 AFGTIGRQLSFODIRIRNDQNGKPYITCTKLSQAANVHSITHTKEYAAQVIERLSS 120
DB 63 AFGTIGRQLSFODIRIRNDQNGKPYITCTKLSQAANVHSITHTKEYAAQVIERLSS 121

RESULT 2
F83714 holo-[acyl]-carrier-protein] synthase BH0518 [imported] - Bacillus halodurans (strain C-1
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: F83714
```

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirata
Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: AB3650; MUID:20512582; PMID:11058132

A;Accession: F83714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-119 <STD>

A;Cross-references: UNIPROT:Q9KEG1; UNIPARC:UPI0000125327; GB:AF001508; GB:BA000004; NIDB:
A;Experimental source: strain C-125

C;Genetic8:

A;Gene: BH0518

A;Superfamily: holo-ACP synthase

[illegible]

RESULT 3
 AE1185
 holo-acyl-carrier protein synthase homolog Imc0885 [imported] - *Listeria monocytogenes* (*C. Species: Listeria monocytogenes*
 C.Date: 27-Nov-2001 #sequence revision 27-Nov-2001 #text_change 09-Jul-2004
 C.Accession: AE1185
 R.Glasser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehli, H. D.; Jones, L.M.; Karet, U.
 Science 294: 849-852, 2001
 A.Authors: Krett, U.; Kuhn, M.; Kunst, F.; Kurupkat, G.; Madueno, E.; Maitouram, A.; Maier, C.; Schlueter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.
 A.Title: Comparative genomics of *Listeria species*.
 A.Reference number: AB1077; MUID:21537279; PMID:11679669
 A.Accession: AE1185
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-118 <GLA>
 A.Cross-references: UNIPROT:O8V8L2; UNIPARC:UP10000054DAF; GB:NC_003210; P1DN:CAC98963.1
 A.Experimental source: strain EGD-e
 C.Genetics:
 A.Gene: Imc0885
 C.Superfamily: holo-ACP synthase

Query Match	48.2%	Score	287	DB 2:	Length	118			
Best Local Similarity	50.9%	Pred	No. 1.2e-21						
Matches	58;	Conservative	21;	Mismatches	35;	Indels	0;	Gaps	0

OY	3	GIGDITTEKRIASNAAGROKPAERILTLRSELDQYVEISEKNNEFLAGRFAKAASFSA	62
		: : : : :	
Db	4	GIGDLMDLERKOVAKENPREIERLTERELTKEPEKEGNKKIFELARFPAKAYAYA	63
		: : : : :	
OY	63	FGTGIGROLSPFDIIRKDQNGKPYLICTKSQAAVHSITTTKEAAAQVITE	116
		: : : : :	
Db	64	NGTGGKHLSFPDVELQVEDGRPHATLVKSGENVFISITTTARSAAAQVITE	117
		: : : : :	

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RESULT 4
AD1543
holo-acyl-carrier protein synthase homolog lln0894 [imported] - Listeria innocua (strain
C|Species: Listeria innocua
C|Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C|Accession: AD1543
R|Glasner, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioche
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
D.; Jones, L.M.; Karst, U.

```

Science 294, 849–852, 2001
A:Authors: Krefetz, J., Kohn, M., Kunst, F., Kurapkai, G., Madueno, E., Maitournam, A., Makarewicz, J., Schlutner, T., Simoes, N., Tillet, A., Vazquez-Boland, J.-A., Voss, H., Weiland, O., C.; Schlutner, T.; Simoes, N.; Tillet, A.; Vazquez-Boland, J.-A.; Voss, H.; Weiland, O.
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1543
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-118 <G1A>
A:Cross-references: UNIPROT:Q9ZDD0; UNIPARC:UP10000125338; GB:AL592022; P1DN:CA69116.1;
A:Experimental source: strain Clp1262
A:Genetics:
A:Gene: lin0884
A:Superfamily: holo-ACP synthase

	47.6%;	Score	283;	DB	2;	Length	118;			
Query Match										
Beat Local Similarity	51.3%	Pred.	No.	3.le-21;						
Matches	59;	Conservative		17;	Mismatches	39;	Indels	0;	Gaps	0;
CY		3 GIGDITELKRIASMAGRQKRFRARILIRSLDDPYLESEKKNFIEFLAGRAAEATSKA	62							
Dd		4 GIGDMIDLDLRVKAQVEKNPRFIERILLTEKETKYEEKSGRKILEFLAGRPAEAAYAKA	63							
CY		63 FGTGIGROLSPQDIETIKRDQNCKRYIILTCLSQAAHVSTITHREYAQAIVVER	117							
Dd		64 NGTFEGKLSTDAEIILOVEDGERPHVMPIKGSETVSVSIHTHRASAQAQTILEQ	118							

RESULT 5
 E89999
 holo-ACP synthase [imported] - Staphylococcus aureus (strain N315)
 C|Species: Staphylococcus aureus
 C|Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
 C|Accession: E89999
 R|Kuroda, M.; Ohts, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Iji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1235-1240, 2001
 A|Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A|Reference number: A89758; MUID:21311952; PMID:11418146
 A|Accession: E89999
 A|Status: Preliminary
 A|Molecule type: DNA
 A|Residues: 1-119 <KUR>
 A|Cross-references: UNIPROT:Q9NS14; UNIPARC:UP10000125346; GB:BA000018; P
 A|Experimental source: strain N315
 C|Genetics:
 A|Gene: dpj
 C|Superfamily: holo-ACP synthase

	Query Match	46.2%;	Score 275;	DB 2;	length 119;
	Best Local Similarity	48.7%;	Pred. No. 2e-20;		
	Matches	Conservative 24;	Mismatches 32;	Indels 4;	Gaps 2;
OY	2 YGIGDITELKRIASMGQRKFRAIRLITSBELDYELS-EKKRNEFLAGRFPAKAAPS	60			
	: :				
Db	3 HGIGVDLLDIRIKVLSKQPKLVERILITKNQKHFNFFTHEORKEIFLAGRFATKEAAPS	62			
OY	61 KAFGTGICRQLSPFDIERIKQNGKPYLICTKLQAAMHVSITTTKEYAAAVIIEER	117			
Db	63 KALSTGKGKVAFNDIDCYNDELCKPXT--DYEGFIIVHSISTHEHYAMSQVVLEK	116			

RESULT 6
C66730
acyl carrier protein synthase [imported] - *Lactococcus lactis* subsp. *lactis* (strain IL14
C.Species: *Lactococcus lactis* subsp. *lactis*
C.Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_09-Jul-2004
C.Accession: C66730
R.Bolotin, A.; Wincker, P.; Manger, S.; Taillon, O.; Malarme, K.; Weisenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A.Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ss
A.Reference number: A86625; MUID:21235186; PMID:11337471

holo-scyl-carriir protein synthase [imported] - Clostridium acetobutylicum
C/Spectra: Clostridium acetobutylicum
C/date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/accession: B96960
R/Mollig, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J.; Daler, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4832-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A/Reference number: A96900; M01D:21559325; EMD:21355325

A:Accession: B96960
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-124 <KUR>
A:Cross-references: UNIPROT:Q97LR5; UNIPARC:UPI000012532F; GB:AEO01437; PIDN:AAK78469.1;
A:Experimental source: Clostridium acetobutylicum ATCC24
C:GeneticCB:
A:Gene: CAC0489
C:Superfamily: holo-ACP synthase

Query Match 37.2%; Score 221.5; DB 2; Length 124;
Best Local Similarity 41.0%; Pred. No. 4,7e-15;
Matches 50; Conservative 25; Mismatches 36; Indels 11; Gaps 3;

Oy 3 GIGDITELKRISAMAGQRKPFAERILTRSELDQYELSEKKRNEFLAGRPAKEAFSA 62
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 4 GVGDVIEIRNVKANIDENYFIETLFSRREI--AYIKAEKTKAQYIAGRPSAKEAVSA 61
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 63 FGTGIGRLSFODIEIRKDQNGKPYIICTKSQA-----AHVSIHTHKEYAAAOVIER 114
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 62 LGTGF-RGFSFKNIETIHDKDGKPIVLNGGARAIAGCYGYOVLSISHREKAIVAV 120
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 115 IE 116
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 121 LE 122

RESULT 11
B72345
holo-(acyl carrier protein) synthase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: B72345
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.

Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: AY2200; MUID:99287316; PMID:10360571
A:Accession: B72345
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-169 <ARN>
A:Cross-references: UNIPROT:Q9WZF6; UNIPARC:UPI0000125349; GB:AEO01741; GB:AEO00512; NID
C:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0692

Query Match 33.9%; Score 201.5; DB 2; Length 169;
Best Local Similarity 42.4%; Pred. No. 6,7e-13;
Matches 50; Conservative 23; Mismatches 30; Indels 15; Gaps 7;

Oy 3 GIGDITELKRISAMAGQRKPFAERILTRSELDQYELSEKKRNEFLAGRPAKEAFSA 62
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 4 GVGDIVLEVER-----PEKFAERILGESEKPLF-LTRKRREFTLAGRPALKEAFKA 55
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy 63 FGTGIGRLSFODIEIRKDQNGKPYIICTKSQA---AVHSIHTHKEYAAAOVIER 117
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 56 LGTGINGH-STDVDF-LESNGKP-VLCVMHDFGFGFNHAHSLSHDR-FAVALVLEK 109
 |::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 12
F71662
holo-(acyl-carrier-protein) synthase (EC 2.7.8.7) RP577 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: F71662
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Almarak, U
Nature 396, 133-140, 1998
A>Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: AF1630; MUID:99039499; PMID:9828893
A:Accession: F71662
A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-126 <AND>
A:Cross-references: UNIPROT:O9ZCK5, UNIPARC:UPI0000125344, GB:AJ235272, GB:AJ235269, NID
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: acps; RP577
C:Superfamily: holo-ACP synthase
C:Keywords: coenzyme A; transferase

Query Match 33.8%; Score 201; DB 2; Length 126;
Best Local Similarity 40.0%; Pred. No. 5, 4e-13;
Matches 48; Conservative 21; Mismatches 45; Indels 6; Gaps 2;

OY 3 GIGDLITELKRIASNAAG-RQKRFAERILTRSELDQYYEISEKKRNEFLAGRFAAKFAFSK 61
DB 4 GVGTDIVDIPREKTLINYQLFPKKIILAKELKOPTLNTKTHATFLARFSAKEAVSK 63

62 AFGTIGIRGLSPDIEIRKDNGKPYI-----ICTKLQAQAAVHSITHTKEVAAGVIE 116
DB 64 AFGVGIRGINKFDITLLNDNLGKPRVEISSHYTNKLAEPNHLISDDYPICIAPAITE 123

RESULT 13
AF0356
holo-[acyl-carrier protein] synthase (EC 2.7.8.7) [imported] - Yersinia pestis (strain CC
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #ext_change 09-Jul-2004
C:Accession: AF0356
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchell, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Farrag, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, L
Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0356
A>Status: preliminary
M:Molecule type: DNA
A:Residues: 1-126 <KUR>
A:Cross-references: UNIPROT:O8ZCP5, UNIPARC:UPI000012534E, GB:AL590842, PIDN:CAC92177.1,
C:Genetics:
A:Gene: acps
C:Superfamily: holo-ACP synthase
C:Keywords: coenzyme A; transferase

Query Match 33.7%; Score 200.5; DB 2; Length 126;
Best Local Similarity 39.0%; Pred. No. 6e-13;
Matches 48; Conservative 21; Mismatches 43; Indels 11; Gaps 3;

OY 3 GIGDLITELKRIASMAAG-RQKRFAERILTRSELDQYYEISEKKRNEFLAGRFAAKFAFSK 61
DB 5 GIGTDIVEISRQDAVERTERLARLRILSPSEWQHQQ--HQQPVFLARKFAVKKAAPK 62

62 AFGTIGIRGLSPDIEIRKDNGKPYI-----ICTKLQAQAAVHSITHTKEVAAGV 113
DB 63 AFGTIGIRGLAENQEVVDALGKPTLRHSPAELAVALGVSLHTVLADDERRYACATV 122

OY 114 VTE 116
DB 123 ITE 125

RESULT 14
E91057
hypothetical protein ECS3429 [imported] - Escherichia coli (strain O157:H7, substrain RH)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #ext_change 09-Jul-2004
C:Accession: E91057
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gesawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E91057

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <HA>
A:Cross-references: UNIPROT:O8XA39, UNIPARC:UPI00001654C5, GB:BA000007, PDB:BA836852.1
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC63429
C:Superfamily: holo-ACP synthase

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CC represents B. subtilis ACPS used to grow ACP/ACPS complex crystals
XX
SQ Sequence 120 AA;

Query Match 100.0%; Score 595; DB 5; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.9e-63;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 60
DB 1 AVGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 60
QY 61 KAFGTGIGRQLSFODIEIRKQNGKPYIITCTLSQAAVHSITHTKEYAAAQVIERLSS 120
DB 61 KAFGTGIGRQLSFODIEIRKQNGKPYIITCTLSQAAVHSITHTKEYAAAQVIERLSS 120

RESULT 2

ID AAY88389 standard; protein; 121 AA.

XX AAY88389;

DT 25-JUL-2000 (first entry)

DE B-ydcb essential bacterial protein amino acid sequence.

XX Bacterial gene; B-ydcb; Streptococcus pneumoniae; antibacterial compound;
KW acyl carrier protein synthase; identify; bacterial infection; treatment.

XX Bacillus subtilis.

OS WO200018952-A1.

XX 06-APR-2000.

XX 30-SEP-1999; 99WO-US022666.

XX 30-SEP-1998; 98US-00163446.

XX (MILL-) MILLENNIUM PHARM INC.

XX Fritz C, Youngman P, Guzman L;

XX WPI; 2000-303457/26.

DR N-PSDB; AAA13271.

PT Identifying new antibacterial agents particularly against Streptococcus
PT pneumoniae, uses S-ydcb polypeptide from S. pneumoniae and B-ydcb
PT polypeptide from Bacillus subtilis.

PS Claim 17; Fig 2; 58pp; English.

CC This sequence represents the essential bacterial protein B-ydcb from
CC Bacillus subtilis. B-ydcb is an ortholog of the S-ydcb from Streptococcus
CC pneumoniae. The gene encodes a protein which has structural
CC characteristics of acyl carrier protein synthase and displays synthase
CC activity in vitro. The protein is used in a method for identifying an
CC antibacterial agent, which comprises contacting an S-ydcb or B-ydcb
CC polypeptide with a test compound and detecting an interaction between the
CC polypeptide and the test compound, where the interaction indicates that
CC the compound is an antibacterial compound. Antibacterial agents
CC identified using the method may be used to treat a bacterial infection,
CC especially Streptococcus pneumoniae in mammals, especially a human or
CC rodent. The method can be configured for high throughput screening of
CC numerous candidate antibacterial agents, and identified agents should
CC have a broad spectrum of antibacterial activity

XX Sequence 121 AA;

Query Match 99.3%; Score 591; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.9e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 61
DB 3 YGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 62
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIITCTLSQAAVHSITHTKEYAAAQVIERLSS 120
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIITCTLSQAAVHSITHTKEYAAAQVIERLSS 121

RESULT 3

ID AAM52130 standard; protein; 121 AA.

XX AAM52130;

DT 01-FEB-2002 (first entry)

DE Bacillus subtilis ACPS.

XX Bacillus subtilis; ACPS; acyl carrier protein synthase; active site;

KW protein coordinate data; CoA binding site; X-ray crystallography;

XX Swiss Protein P96618.

OS Bacillus subtilis.

XX WO200155340-A2.

XX 26-JAN-2001; 2001WO-US002732.

XX 28-JAN-2000; 2000US-0178639P.

XX (AMHP) AMERICAN HOME PROD CORP.

XX (MILL-) MILLENNIUM PHARM INC.

XX Parrie KD, Somers WS, Tam AS, Lin LL, Stahl ML;

XX WPI; 2001-476201/51.

PT Novel crystallized acyl carrier protein synthase enzyme used to identify
PT an activator or inhibitor of a molecule or complex comprising a CoA
PT binding site, and to determine the molecular structure of a molecule or
PT complex.

PS Disclosure; Fig 8; 181pp; English.

CC The invention relates to a crystallized acyl carrier protein synthase
CC (ACPS) enzyme used to identify an agent that interacts with the active
CC site, to identify an activator or inhibitor of a molecule or molecular
CC complex comprising a CoA binding site and to determine the molecular
CC structure. The present sequence is that of the Bacillus subtilis ACPS

XX Sequence 121 AA;

Query Match 99.3%; Score 591; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.9e-63;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 61
DB 3 YGIGDITELKRIASMGROKRFARILITRSELDQYELSEKRNKNEFLAGFAKAEFSK 62
QY 62 AFGTIGRQLSFODIEIRKQNGKPYIITCTLSQAAVHSITHTKEYAAAQVIERLSS 120
DB 63 AFGTIGRQLSFODIEIRKQNGKPYIITCTLSQAAVHSITHTKEYAAAQVIERLSS 121

RESULT 4

ID ABU18305 standard; protein; 119 AA.

XX ABU18305

AC ABU18305;
 XX 19-JUN-2003 (first entry)
 DT
 DE Protein encoded by Prokaryotic essential gene #3832.
 XX
 KM Antisense, prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Bacillus anthracis.
 XX
 PN MO20027183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 XX
 PR 06-SEP-2001; 2001US-00948993.
 XX
 PR 25-OCT-2001; 2001US-0342823P.
 XX
 PR 08-FEB-2002; 2002US-00072851.
 XX
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Wang L, Zamudio C, Malone C, Haeelbeck R, Ohlsen KU, Zykind JW;
 PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
 PI
 PI MPI; 2003-029926/02.
 DR N-PSDB; ACA22175.
 DR
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 46229; 1766bp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation; (7) identifying a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 119 AA;

Query Match 51.1%; Score 304; DB 6; Length 119;
 Best Local Similarity 54.2%; Prod. No. 2.5e-28;
 Matches 64; Conservative 20; Mismatches 32; Indels 2; Gaps 1;

OY 3 GIGDITELKRIASWAGROKFAERILTRSELDQYELSEKRNKEFLAGFAEAFSKA 62
 DB 4 GIGDITELKRIEKMLOGKLFMERILTENRANVAKLKGSRLLTEFVAGRRPAEAVSKA 63
 OY 63 FGCTGIGROLSPQDIEIRKDNQKPEYIICTKLSQAAVHSITHTYEVAAQVIERLSS 120
 DB 64 VGTGIGKEVSTLDEVRNDRGKPIILITS--TEHIVHLSISHSKFEFAVQVLESSSS 119

RESULT 5
 ABB47581
 ID ABB47581 standard; protein; 118 AA.
 XX
 AC ABB47581;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #285.
 XX
 KM Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KM vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 XX
 PN MO200177335-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 11-APR-2001; 2001WO-FR001118.
 XX
 PR 11-APR-2000; 2000FR-00004629.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Buchrieser C, Frangoul L, Couve E, Ruenick C, Fslhi H, Dehoux P;
 PI Dusurget O, Chetouni F, Nedjari H, Glaeser P, Kunst F, Coessart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Doman E, Hain T, Berche P, Chablit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 PI Madeno E, De Pablos B, Weiland J, Kaerst U, Entian K, Haut J;
 PI Rose M, Voss H;
 XX
 DR MPI; 2002-010914/01.
 XX
 PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 PT and prevention of Listeria and related bacterial infections, and related
 PT polypeptides.
 XX
 PS Claim 6; SEQ ID NO 286; 192pp; French.
 XX
 CC The present invention relates to the genome sequence of Listeria
 CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in *L.*
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising antisense
 CC antibodies, identification of *L. monocytogenes* and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccine compositions for the treatment or prevention of infections by *L.*
 CC monocytogenes and related organisms. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 118 AA;

Query Match 48.2%; Score 287; DB 5; Length 118;
Best Local Similarity 50.9%; Pred. No. 2.8e-26;
Matches 58; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC XX

SQ Sequence 118 AA;

ABU32572
ID ABU32572 standard; protein, 118 AA.
XX
AC ABU32572;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #18099.
XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS *Listeria monocytogenes*.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
XX
PR 06-SEP-2001; 2001US-00948993.
XX
PR 25-OCT-2001; 2001US-0342923P.
XX
PR 08-FEB-2002; 2002US-00072851.
XX
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR MPI: 2003-029926/02.
XX
DR N-PSDB; ACA36442.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 60496; 1766bp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC XX

SQ Sequence 118 AA;

ABP39429
ID ABP39429 standard; protein, 124 AA.
XX
AC ABP39429;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4274.
XX
KM Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
XX antibacterial; gene therapy.
XX
OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-00134001.
XX
PR 14-AUG-1997; 97US-0055779P.
XX
PR 08-NOV-1997; 97US-0064964P.
XX
PA (GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR MPI: 2002-381255/41.
XX
DR N-PSDB; ABN91974.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS Disclosure; SEQ ID NO 4274; 267bp; English.
XX
XX ABN90558 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The *S. epidermidis* sequences have
CC antibacterial activity and can be used in gene therapy. The sequences can
CC also be used in the diagnosis and treatment of bacterial infections,
CC particularly *S. epidermidis* infections. The sequences can be used to
CC screen for compounds able to interfere with the *S. epidermidis* life cycle
CC or inhibit *S. epidermidis* infection. N.B. The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site


```

XX      27-SEP-2001.
PD
XX
XX      21-MAR-2001; 2001WO-US009180.
PF
XX
XX      21-MAR-2000; 2000US-0191078P.
PR
XX      23-MAY-2000; 2000US-0206848P.
PR
XX      26-MAY-2000; 2000US-0207727P.
PR
XX      23-OCT-2000; 2000US-0242578P.
PR
XX      27-NOV-2000; 2000US-0253625P.
PR
XX      22-DEC-2000; 2000US-0257931P.
PR
XX      16-FEB-2001; 2001US-0269308P.
PA
XX      (ELIT-) ELITRA PHARM INC.
PI
XX      Haasbeek R, Ohlsen KL, Zyskind JW, Wall D, Treweek JD, Carr GT,
PI
XX      Yamamoto RT, Xu HH;
DR
XX      WPI, 2001-611495/70.
DR
XX      N-PsDB, AAS51704.
PT
XX      New polynucleotides for the identification and development of
PT
XX      antibiotics, comprise sequences of antisense nucleic acids.
PS
XX      Example 3; SEQ ID NO 5341; 511BP; English.
XX
XX      The invention relates to antisense inhibitors of genes essential to
XX      prokaryotic cellular proliferation, their use in identifying the genes,
XX      their use in the discovery of novel antibiotics, the essential genes,
XX      themselves and the encoded proteins. The prokaryotes used are Escherichia
XX      coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX      Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX      useful for the identification of potential new targets for antibiotic
XX      development. The antisense nucleic acids can also be used to identify
XX      proteins used in proliferation, to express these proteins, and to obtain
XX      antibodies capable of binding to the expressed proteins. The proteins can
XX      be used to screen compounds in rational drug discovery programmes. The
XX      antisense nucleic acid sequence is also useful to screen for homologous
XX      nucleic acids which are required for cell proliferation in a wide variety
XX      of organisms. The present sequence represents an essential prokaryotic
XX      cellular proliferation protein. Note: The sequence data for this patent
XX      did not form part of the printed specification, but was obtained in
XX      electronic format directly from WIPO at
XX      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 119 AA;

Query Match          46.6%; Score 277; DB 4; Length 119;
Best Local Similarity 48.7%; Pred. No. 4, 6e-25;
Matches   57; Conservative    25; Mismatches   31; Indels     4; Gaps     2

OY      2 YGIGDITELKRIASMAGROKRFAERILTRSELIDQYEES-EKKNEPLAIGRPAAKEAFS 60
        |||::||:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB       3 HGIQDLLEIDIRIKVLYSKOPKLVEILLTKNEOHKNFNFTPHQRKFEPFATGEARS 62
        |||::||:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      61 KAFVGICRGQLSRFDIEIRKDNGKRYIICTLSQAAYVSTTHTEVAADAVIER 117
        |||::||:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB       63 KALGTGLGRHVAFNIDICYNDELGRPKT--DYEGTFIVASTSHTEQVAMSOVLEAK 116
        |||::||:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 14
AAU36808
ID      AAU36808 standard, protein, 119 AA.
XX
XX      AAU36808;
AC
XX      14-FEB-2002 (first entry)
DT
XX
DE      Staphylococcus aureus cellular proliferation protein #978.
KW      Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX      antibacterial; drug design.
XX
```

```
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
XX PR 23-MAY-2000; 2000US-0206848P.
XX PR 26-MAY-2000; 2000US-0207727P.
XX PR 23-OCT-2000; 2000US-0242578P.
XX PR 27-NOV-2000; 2000US-0253625P.
XX PR 22-DEC-2000; 2000US-0257931P.
XX PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KJ, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI: 2001-611495/70.
XX N-PSTB; AAS54667.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Example 3; SEQ ID NO 12401; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 119 AA:
Query Match 46.6%; Score 277; DB 4; Length 119;
Best Local Similarity 48.7%; Pred. No. 4.6e-25;
Matches 57; Conservative 25; Mismatches 31; Indels 4; Gaps 2;
OY 2 YGIGDIDELKRIASMAGRQKRFAERITRSSELDQYYLS-EKKRMFLAGRFKAKEAFS 60
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 3 HGIQGDLLEIRIKVLKYKQPLVERILITKNQKHFNFTFTEQRKIETELAGRFAKTKEFS 62
HGIQGDLLEIRIKVLKYKQPLVERILITKNQKHFNFTFTEQRKIETELAGRFAKTKEFS
OY 61 KAFGTGIGROSLFDODIEIRKDQNGKPYIITCKLSQAAVHSITHTKEYAANQVIAR 117
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 63 KALGTGLGKHAVFNDICYNDELGRPKI---DYEGFIHVHSISHTEQYAMSOVVLEK 116
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
RESULT 15
AAB14979
ID AAB14979 standard; protein; 119 AA.
AC AAB14979;
XX
DT 01-DEC-2000 (first entry)
XX
DE Staphylococcus aureus phosphopantetheinyl transferase protein Acps.
XX
```


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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:54:50 ; Search time 5.64179 Seconds
(without alignments)
102.397 Million cell updates/sec

Title: US-10-717-138-1

Perfect score: 397
Sequence: 1 GELGADTLERVTYKTIIVDL.....EDAKIATVGAIVNTIQNOQ 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB pep:*
2: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB pep:*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB pep:*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB pep:*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB pep:*
6: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB pep:*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB pep:*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	54.7	76	6	US-10-467-657-4016 Sequence 4016, Ap
2	217	54.7	78	6	US-10-467-657-3996 Sequence 3996, Ap
3	217	54.7	78	6	US-10-467-657-7044 Sequence 7044, Ap
4	135	34.0	178	6	US-10-821-234-1052 Sequence 1052, Ap
5	94.5	23.8	2910	7	US-11-087-100-2 Sequence 2, Appl1
6	94.5	23.8	2910	7	US-11-087-084-2 Sequence 2, Appl1
7	94.5	23.8	2910	7	US-11-087-085-2 Sequence 2, Appl1
8	91.5	23.0	86	7	US-11-087-100-13 Sequence 13, Appl1
9	91.5	23.0	86	7	US-11-087-084-13 Sequence 13, Appl1
10	91.5	23.0	86	7	US-11-087-085-13 Sequence 13, Appl1
11	73.5	18.5	371	6	US-10-467-6628-41 Sequence 214, App
12	68	17.1	697	7	US-11-074-176-214 Sequence 96, Appl
13	65.5	16.5	412	7	US-11-082-389-96 Sequence 96, Appl
14	62.5	15.7	642	6	US-10-467-657-5900 Sequence 5900, Ap
15	62.5	15.6	1061	7	US-11-059-814-18 Sequence 18, Appl
16	61.5	15.5	530	6	US-10-858-730-67 Sequence 67, Appl
17	61	15.4	1001	6	US-10-467-6628-81 Sequence 81, Appl
18	60	15.1	327	7	US-11-129-143-91 Sequence 91, Appl
19	60	15.1	327	7	US-11-075-185-10 Sequence 10, Appl
20	59.5	15.0	1766	7	US-11-075-185-10 Sequence 10, Appl
21	59	14.9	188	6	US-10-793-626-592 Sequence 592, App
22	59	14.9	128	7	US-11-105-864-4 Sequence 4, Appl1
23	59	14.9	274	6	US-10-467-657-2140 Sequence 2140, App
24	59	14.9	449	6	US-10-485-517-272 Sequence 272, App
25	58.5	14.7	269	6	US-10-793-626-2472 Sequence 2472, App

26	58.5	14.7	345	6	US-10-485-517-314 Sequence 314, App
27	58.5	14.7	353	7	US-10-793-626-2730 Sequence 2730, Ap
28	58.5	14.7	431	6	US-11-060-920-4 Sequence 4, Appl1
29	58.5	14.7	872	7	US-11-077-550-145 Sequence 145, App
30	58.5	14.7	879	7	US-11-077-550-143 Sequence 143, App
31	58.5	14.7	887	7	US-11-077-550-147 Sequence 147, App
32	58.5	14.7	1315	7	US-11-077-550-141 Sequence 141, App
33	58	14.6	424	6	US-10-793-626-2296 Sequence 2296, App
34	58	14.6	484	6	US-10-467-657-6816 Sequence 6816, App
35	58	14.6	1196	6	US-10-613-744-9 Sequence 9, Appl1
36	57.5	14.5	597	6	US-10-467-657-3020 Sequence 3020, App
37	57.5	14.5	610	6	US-10-858-730-292 Sequence 292, App
38	57.5	14.5	720	6	US-10-793-626-2058 Sequence 2058, App
39	57.5	14.5	1804	6	US-10-513-786-2 Sequence 1, Appl1
40	57.5	14.5	3704	6	US-10-821-234-1573 Sequence 1, Appl1
41	57	14.4	635	6	US-10-821-234-1573 Sequence 1573, App
42	57	14.4	724	6	US-10-821-234-1506 Sequence 1506, App
43	57	14.4	1163	7	US-11-044-899-2 Sequence 2, Appl1
44	57	14.4	1163	7	US-11-044-899-30 Sequence 30, Appl1
45	56.5	14.2	341	6	US-10-793-626-1278 Sequence 1278, App

ALIGNMENTS

```
RESULT 1
US-10-467-657-4016
; Sequence 4016, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4016
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4016

Query Match      54.7%; Score 217; DB 6; Length 76;
Best Local Similarity 66.2%; Pred. No. 9,1e-16;
Matches 45; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY      10 ERYTKTIIVRLGVADVADKLEAFKEDLGADSLDVELVMELEDFDEPDEISDAEKIAT 69
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      4 QQVKKIIAQLGVADVADKLEAFKEDLGADSLDVELVMELEDFDEPDEISDAEKIAT 63

QY      70 VGDVAVNYI 77
      |::|::|
DB      64 VGLAIDYI 71

RESULT 2
US-10-467-657-3996
; Sequence 3996, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

```
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3996
LENGTH: 78
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3996

Query Match
Best Local Similarity 54.7%; Score 217; DB 6; Length 78;
Matches 45; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Db
10 ERYTKIIVRLGVDEADVLEASFKEIDLGADSLDVVELVMELEDEPFDEISDEDAEKIAT 69
6 QGVKIIAEQLGVNEADVKNESFFQDGLGADSLDVVELVMELEAFGEIIPDEDAEKITT 65
QY 70 VGDVAVNYI 77
66 VOLAIDYI 73
Db

RESULT 3
US-10-467-657-7044
Sequence 7044, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 7044
LENGTH: 78
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7044

Query Match
Best Local Similarity 54.7%; Score 217; DB 6; Length 78;
Matches 45; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Db
10 ERYTKIIVRLGVDEADVLEASFKEIDLGADSLDVVELVMELEDEPFDEISDEDAEKIAT 69
6 QGVKIIAEQLGVNEADVKNESFFQDGLGADSLDVVELVMELEAFGEIIPDEDAEKITT 65
QY 70 VGDVAVNYI 77
66 VOLAIDYI 73
Db

RESULT 4
US-10-821-234-1052
Sequence 1052, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
```

```
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0
SEQ ID NO 1052
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1052

Query Match
Best Local Similarity 34.0%; Score 135; DB 6; Length 178;
Matches 30; Conservative 17; Mismatches 33; Indels 0; Gaps 0;

Db
2 PLGSADTLERYTKIIVRLGVDEADVLEASFKEIDLGADSLDVVELVMELEDEPFDEISD 61
95 PLTEGIODRVLVYLYKLYDKIDPEKLSVSHFMKDLGSLDQVEIIMAMDEDFGFELPD 154
QY 62 EDAEKIATVGDVAVNYIONQ 81
155 IDAEKLMCPGEIVDYIDKK 174
Db

RESULT 5
US-11-087-100-2
Sequence 2, Application US/11087100
Publication No. US20050266440A1
GENERAL INFORMATION:
APPLICANT: Metz, James
APPLICANT: Barclay, William
APPLICANT: Flatt, James
APPLICANT: Kuner, Jerry
TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORF of a PUFa Polyketide Synthase
FILE REFERENCE: 2997-29
CURRENT APPLICATION NUMBER: US/11/087,100
CURRENT FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: 09/231,899
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/284,066
PRIOR FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/298,796
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/323,269
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.3
SEQ ID NO 2
LENGTH: 2910
TYPE: PRT
ORGANISM: Schizochytrium sp.
US-11-087-100-2

Query Match
Best Local Similarity 23.8%; Score 94.5; DB 7; Length 2910;
Matches 26; Conservative 18; Mismatches 26; Indels 13; Gaps 3;

Db
2 PLGSADTLERYTKIIVRLGVDEADVLEASFKEIDLGADSLDVVELVMELEDEPFDEISD 53
1114 PAVSNELEKAEYVMEVLAKTGYETDMTEADMELET---ELGIDSIKVELISVQA 1169
QY 54 EFDMEISDEDA-EKIATVGDVAVN 75
1170 MLNVEAKVDALSRRTVGEVNV 1192
Db

RESULT 6
US-11-087-084-2
Sequence 2, Application US/11087084
Publication No. US20050273883A1
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		23.8%	Score 94.5;	DB 7;	Length 2910;
Query Match		31.3%;	Pred. No. 0.12;		
Best Local Similarity		18;	Mismatches 26;	Indels 13;	Gaps 3;
Matches					
OY	2	PLGSAADTIERTKIIVRLGYD	----	EADVKLEAFKEDIGASDLVDELVMETLED	53
		: :		: : :	
Db	1114	PAVSNELLEKAEKVMEVTLAAKTGEYENDIMADMELFT	---	ELGIDISIKREKELLISEVOA	1169
OY	54	EFDMEISDEDA-EKIATVGDAVN	75		
Db	1170	MLNVEAKQVDALSRTRTVGEAVN	1192		
		::: : :			

Query Match	23.8%;	Score 94.5;	DB 7;	Length 2910;
Best Local Similarity	31.3%;	Pred. No. 0.12;		
Matches 26;	Conservative 18;	Mismatches 26;	Indels 13;	Gaps 3;

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Query Match      23.0%; Score 91.5; DB 7; Length 86;
Best Local Similarity 31.2%; Pred. No. 0.0033;
Matches 25; Conservative 18; Mismatches 24; Indels 13; Gaps 3;

Oy      5 SADTLERTKTIIVRLGVD-----EADVKLEASFKEKDAGSDSLDVELVMELEDEFD 56
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      3 SNEELERKEIYVMEXVLAAKTGYETDMIEADMELT----ELGIDSIKRVELISLSEVGQMLN 58

Oy      57 MEISDEDA-EKIATVGDVN 75
        : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     59 VEAKDVDA LSRRTVGEVVN 78

RESULT 9
US-11-087-084-13
? Sequence 13, Application US/11087084
? Publication No. US2005027383A1
? GENERAL INFORMATION:
? APPLICANT: Metz, James
? APPLICANT: Barclay, William
? APPLICANT: Flatt, James
? APPLICANT: Kumer, Jerry
? TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORF1 of a PUFA Polyketide Synthase
? FILE REFERENCE: System and Uses Thereof
? FILE REFERENCE: 2957-29
? CURRENT APPLICATION NUMBER: US/11/087,084
? CURRENT FILING DATE: 2005-03-21
? PRIOR APPLICATION NUMBER: 09/231,899
? PRIOR FILING DATE: 1999-01-14
? PRIOR APPLICATION NUMBER: 60/284,066
? PRIOR FILING DATE: 2001-04-16
? PRIOR APPLICATION NUMBER: 60/298,796
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/323,269

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;; PRIOR FILING DATE: 2001-09-18
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 13
;; LENGTH: 86
;; TYPE: PRT
;; ORGANISM: Schizochytrium sp.
US-11-087-084-13

Query Match 23.0%; Score 91.5; DB 7; Length 86;
Best Local Similarity 31.2%; Pred. No. 0.0033;
Matches 25; Conservative 18; Mismatches 24; Indels 13; Gaps 3;

QY 5 SADTLERVKTIIVDRLGVD-----EADVKLEASFKEKEDLGADSLDVVELVMELEDED 56
DB 3 SHELLEKATVMEVLAATGYETDMIEADMELET---ELGIDSIKRVELLSEVOAMLN 58
QY 57 MEISDEDA-EKATVGDVAVN 75
DB 59 VEAKVDALSRRTTGEVAVN 78

RESULT 10

US-11-087-085-13
;; Sequence 13, Application US/11087085
;; Publication No. US20050273884A1
;; GENERAL INFORMATION:
;; APPLICANT: Metz, James
;; APPLICANT: Barclay, William
;; APPLICANT: Platt, James
;; APPLICANT: Kumer, Jerry
;; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
;; TITLE OF INVENTION: System and Uses Thereof
;; FILE REFERENCE: 2997-23
;; CURRENT APPLICATION NUMBER: US/11/087,085
;; CURRENT FILING DATE: 2005-03-21
;; PRIOR APPLICATION NUMBER: 09/231,899
;; PRIOR FILING DATE: 1999-01-14
;; PRIOR APPLICATION NUMBER: 60/284,066
;; PRIOR FILING DATE: 2001-04-16
;; PRIOR APPLICATION NUMBER: 60/298,796
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/323,269
;; PRIOR FILING DATE: 2001-09-18
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 13
;; LENGTH: 86
;; TYPE: PRT
;; ORGANISM: Schizochytrium sp.
US-11-087-085-13

Query Match 23.0%; Score 91.5; DB 7; Length 86;
Best Local Similarity 31.2%; Pred. No. 0.0033;
Matches 25; Conservative 18; Mismatches 24; Indels 13; Gaps 3;

QY 5 SADTLERVKTIIVDRLGVD-----EADVKLEASFKEKEDLGADSLDVVELVMELEDED 56
DB 3 SHELLEKATVMEVLAATGYETDMIEADMELET---ELGIDSIKRVELLSEVOAMLN 58
QY 57 MEISDEDA-EKATVGDVAVN 75
DB 59 VEAKVDALSRRTTGEVAVN 78

RESULT 11

US-10-467-962B-41
;; Sequence 41, Application US/10467962B
;; Publication No. US20050246784A1
;; GENERAL INFORMATION:
;; APPLICANT: Plesch, Gunnar
;; APPLICANT: Blau, Astrid
;; APPLICANT: Daeschner, Klaus

;; APPLICANT: Klein, Mathieu
;; TITLE OF INVENTION: Identification of Herbicidically Active Substances
;; FILE REFERENCE: 2000 857
;; CURRENT APPLICATION NUMBER: US/10/467,962B
;; CURRENT FILING DATE: 2003-08-14
;; PRIOR APPLICATION NUMBER: PCT/EP02/01466
;; PRIOR FILING DATE: 2002-02-13
;; NUMBER OF SEQ ID NOS: 109
;; SOFTWARE: PatentIn Vers. 2.0
;; SEQ ID NO 41
;; LENGTH: 371
;; TYPE: PRT
;; ORGANISM: Arabidopsis thaliana
US-10-467-962B-41

Query Match 18.5%; Score 73.5; DB 6; Length 371;
Best Local Similarity 26.8%; Pred. No. 1.2;
Matches 26; Conservative 19; Mismatches 33; Indels 19; Gaps 3;

QY 4 GSADTLERVRK-----IIVRLGVDAADVLEASFKEKEDLGADSLDV-----VELV 48
DB 274 GSDBEIERLRKFRACIGLFGVVDILDYTKSSKELGKTACKDLIADKLTPTKIMGLEKS 333
QY 49 MELEDEPFMEISDE---DAEKIATVGDVAVNYIQNOQ 81
DB 334 REPAKLNREARDQILGFSDKVAPLALANYIAYRQ 370

RESULT 12

US-11-074-176-214
;; Sequence 214, Application US/11074176
;; Publication No. US20050250135A1
;; GENERAL INFORMATION:
;; APPLICANT: Klaenhammer, Todd R.
;; APPLICANT: Russell, William M.
;; APPLICANT: Altermann, Eric
;; APPLICANT: McAlliffe, Olivia
;; APPLICANT: Perill, Andrea Azcarate
;; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
;; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
;; FILE REFERENCE: 5051-694
;; CURRENT APPLICATION NUMBER: US/11/074,176
;; CURRENT FILING DATE: 2005-03-07
;; PRIOR APPLICATION NUMBER: 60/551,161
;; PRIOR FILING DATE: 2004-03-08
;; NUMBER OF SEQ ID NOS: 381
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 214
;; LENGTH: 697
;; TYPE: PRT
;; ORGANISM: Lactobacillus acidophilus
US-11-074-176-214

Query Match 17.1%; Score 68; DB 7; Length 697;
Best Local Similarity 27.6%; Pred. No. 9.2;
Matches 21; Conservative 14; Mismatches 27; Indels 14; Gaps 2;

QY 2 PLGSADTLERVKTI-----VDRLGVDADVLEASFKEKEDLGADSLDVVELVMELEDED 53
DB 167 PIGSADTFEGVADILNNVADIDYEDKLGSKWMDTVFPDVEYKEAEKRRALIEAVADVDD 226
QY 54 EF-----DMEISDED 63
DB 227 NIMKYLGGERSINDE 242

RESULT 13

US-11-082-389-96
;; Sequence 96, Application US/11082389
;; Publication No. US20050244935A1
;; GENERAL INFORMATION:
;; APPLICANT: Pompejus, Markus
;; APPLICANT: Kroger, Burkhard

APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Habeshauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-131CPCN
CURRENT APPLICATION NUMBER: US/11/082,389
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930487.4
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19930489.0
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931549.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931550.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932134.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 446
SEQ ID NO 96
LENGTH: 412
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-082-389-96

Query Match 16.5%; Score 65.5; DB 7; Length 412;
Best Local Similarity 30.3%; Pred. No. 8.6;
Matches 20; Conservative 8; Mismatches 19; Indels 19; Gaps 2;
QY 10 ERTKTIIVRLGVDEADVLEKLEAFKEDLGADSLDVLELWLEDEFDEPMEISDDAEKIAI 69
DB 242 ERYARVVAELGVDEVAELMP-----DKLEIVELQAO-----GRVVM 282
QY 70 VGDVAV 75
DB 283 VGDGVN 288

RESULT 14
US-10-467-657-5900
Sequence 5900, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIIGNANI Vega
APPLICANT: MONACT Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5900
LENGTH: 642
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5900

Query Match 15.7%; Score 62.5; DB 6; Length 642;
Best Local Similarity 27.7%; Pred. No. 29;
Matches 23; Conservative 11; Mismatches 46; Indels 3; Gaps 1;
QY 2 PLGSADTLERYTKIIVRLGVDEADVLEKLEAFKEDLGADSLDVLELWLEDEFDEPME 58
DB 157 PGSIAMEILELKEICKDEIRVDEVEAIIIDPREVLNLELGLHLETTAPEKPSNDNSDEN 216
QY 59 ISDEDAEKIATVGDVNTIQNDQ 81
DB 217 EDDSESEDADEISANLAELEKQ 239

RESULT 15
US-11-059-814-18
Sequence 18, Application US/11059814
Publication No. US20050272650A1
GENERAL INFORMATION:
APPLICANT: University of South Florida
APPLICANT: Monapetra, Shyam
TITLE OF INVENTION: Materials and Methods for Treatment of Inflammatory and Cell
TITLE OF INVENTION: Proliferation Disorders
FILE REFERENCE: USF-215PTC2
CURRENT APPLICATION NUMBER: US/11/059,814
CURRENT FILING DATE: 2005-02-17
PRIOR APPLICATION NUMBER: 60/521,072
PRIOR FILING DATE: 2004-02-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 1061
TYPE: PRT
ORGANISM: Homo sapiens
US-11-059-814-18

Query Match 15.6%; Score 62; DB 7; Length 1061;
Best Local Similarity 29.3%; Pred. No. 61;
Matches 22; Conservative 10; Mismatches 29; Indels 14; Gaps 2;
QY 1 GPLGSADTLERYTKIIVRLGVDEADVLEKLEAFKEDLGADS--LDVLELWLEDEFDEPME 58
DB 864 GETVQAELAFDSVTIYPSDIVGFTA-----LSAESTPMQVVTLLNDLYTCFDAV 911
QY 59 ISDEDAEKIATVGDGA 73
DB 912 IDNFVYKVEITIGDA 926

Search completed: December 21, 2005, 14:13:51
Job time : 6.64179 secs

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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:49:45 / Search time 89.8657 Seconds
(without alignments)
376.608 Million cell updates/sec

Title: US-10-717-138-1

Perfect score: 397
Sequence: 1 GPLGSADTLERYTKIIVDR.....EDAEKATVGDVAVNYIONQ 81

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubppae/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppae/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	100.0	81	3	US-09-770-834-1
2	397	100.0	81	4	US-10-717-138-1
3	307	77.3	80	4	US-10-282-122A-46208
4	284	71.5	77	4	US-10-282-122A-60882
5	254	64.0	77	4	US-09-815-242-10973
6	254	64.0	76	4	US-10-282-122A-58089
7	249	62.7	76	4	US-10-282-122A-67443
8	239	60.2	110	4	US-10-282-122A-77373
9	238	59.9	77	4	US-10-282-122A-70919
10	238	59.9	77	4	US-10-282-122A-71791
11	238	59.9	79	4	US-10-724-972A-5601
12	236	59.4	77	4	US-10-282-122A-51523
13	234	58.9	77	3	US-09-815-242-12802
14	234	58.9	77	3	US-09-815-242-13101
15	234	58.9	77	4	US-10-282-122A-44414
16	234	58.9	77	5	US-10-857-625-626
17	232	58.4	73	3	US-09-815-242-5462
18	232	58.4	77	3	US-09-815-242-12124
19	227	57.2	79	4	US-10-282-122A-51445
20	226	57.1	78	4	US-10-282-122A-78573
21	225	56.7	104	4	US-10-282-122A-52553
22	223.5	56.3	75	4	US-10-369-493-8522
23	222.5	56.0	72	4	US-10-369-493-7064
24	222.5	56.0	78	4	US-10-369-493-4308
25	222.5	56.0	79	4	US-10-282-122A-47901
26	222.5	56.0	79	4	US-10-282-122A-49501
27	222.5	56.0	79	4	US-10-282-122A-50326

28	222	55.9	78	4	US-10-369-493-132	Sequence 132, App
29	222	55.9	80	5	US-10-501-282-4732	Sequence 4732, Ap
30	220	55.4	75	4	US-10-369-493-21035	Sequence 21035, A
31	220	55.4	82	4	US-10-282-122A-61113	Sequence 61113, A
32	217	54.7	71	4	US-10-369-493-9111	Sequence 9111, Ap
33	217	54.7	76	4	US-10-369-493-10628	Sequence 10628, A
34	217	54.7	78	4	US-10-282-122A-65150	Sequence 65150, A
35	216	54.4	78	4	US-10-369-493-12321	Sequence 12321, A
36	216	54.4	78	4	US-10-282-122A-65580	Sequence 65580, A
37	215	54.2	77	3	US-09-770-834-15	Sequence 15, Appl
38	215	54.2	77	4	US-10-717-138-15	Sequence 15, Appl
39	215	54.2	78	3	US-09-815-242-10127	Sequence 10127, A
40	215	54.2	78	4	US-10-230-331-39	Sequence 39, Appl
41	215	54.2	78	4	US-10-369-493-795	Sequence 795, App
42	215	54.2	78	4	US-10-282-122A-43145	Sequence 43145, A
43	215	54.2	78	4	US-10-282-122A-67855	Sequence 67855, A
44	215	54.2	78	4	US-10-282-122A-72742	Sequence 72742, A
45	215	54.2	78	4	US-10-282-122A-75153	Sequence 75153, A

ALIGNMENTS

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RESULT 1
US-09-770-834-1
; Sequence 1, Application US/09770834
; Publication No. US20030211588A1
; GENERAL INFORMATION:
; APPLICANT: Somers, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14
; CURRENT APPLICATION NUMBER: US/09/770, 834
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/202,466
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-770-834-1
Query Match 100.0%; Score 397; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.7e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPLGSADTLERYTKIIVDRLGVDVADVKLEASFKEDLGADSLDVELVNELEDFPMEIS 60
DB 1 GPLGSADTLERYTKIIVDRLGVDVADVKLEASFKEDLGADSLDVELVNELEDFPMEIS 60
QY 61 DEDAERKATVGDVAVNYIONQ 81
DB 61 DEDAERKATVGDVAVNYIONQ 81
RESULT 2
US-10-717-138-1
; Sequence 1, Application US/10717138
; Publication No. US20040078147A1
; GENERAL INFORMATION:
; APPLICANT: Paritb, Kevin
; APPLICANT: Somers, William
; APPLICANT: Tam, Amy
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
```

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; APPLICANT: Powers, Robert
; APPLICANT: Xu, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
; FILE REFERENCE: 2368/14
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/10/717,138
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/770,834
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-717-138-1

Query Match      100.0%; Score 397; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.7e-35;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GPGSADTLERYTKIIVDRIGVDEADVKLKASFKEDLGADSLDVVELVMELEDFDMEIS 60
Db      1  GPLGSADTLERYTKIIVDRIGVDEADVKLKASFKEDLGADSLDVVELVMELEDFDMEIS 60

Qy      61  DEDAEXIATVGDAVNYIQNQ 81
Db      61  DEDAEXIATVGDAVNYIQNQ 81

RESULT 3
US-10-282-122A-46208
; Sequence 46208, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46208
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-282-122A-46208

Query Match      77.3%; Score 307; DB 4; Length 80;
Best Local Similarity 82.9%; Pred. No. 1.4e-25;
Matches 63; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy      4  GSADTLERYTKIIVDRIGVDEADVKLKASFKEDLGADSLDVVELVMELEDFDMEIS 63
Db      3  GMADVLERVTKIIVDRIGVDEADVLPASFKEDLGADSLDVVELVMELEDFDMEIS 62

Qy      64  AEKIATVGDAVNYIQN 79
Db      63  AEKIATVGDAVNYIES 78

RESULT 4
US-10-282-122A-60882
; Sequence 60882, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60882
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60882

Query Match      71.5%; Score 284; DB 4; Length 77;
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APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Foreyech, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58089
LENGTH: 76
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-282-122A-58089

Query Match          64.0%; Score 254; DB 4; Length 76;
Best Local Similarity 72.2%; Pred. No. 7,le-20;
Matches 52; Conservative 8; Mismatches 12; Indels 0; Gaps 0,

QY      10 ERYTKIIVDRIGVDEADVKLKASFKEDLGADSLDVEELVNELEDFPMEISDEDAAKIAT 69
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB       5 ERVKILIVEGVGVEDEVKCEASFVEDLGDSDLTVIELVMALFEFPFIEIDPEAEAKITT 64

QY      70 VGDANYTQNQQ 81
        |:::|||
DB       65 VGSALDVQNNQ 76

RESULT 7
US-10-282-122A-67443
Sequence 67443, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

```

; PRIOR APPLICATION NUMBER: 60/230,335

;; PRIOR APPLICATION NUMBER: 80/237,351
;; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/230,335

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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70919
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70919

Query Match      59.9%; Score 238; DB 4; Length 77;
Best Local Similarity 67.1%; Pred. No. 3.8e-18;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTLERVTKIIVRLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAEK 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 ENPDKVKDIIVRLGVDAVDKVTEDASFKDLDGADSLDIAEVLVMELEDFGTETIPDEBAEK 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 IATVGDAVNYION 79
    | | | | | | | | | | :
DB 62 INTVGDAVKYINS 74

RESULT 10
US-10-282-122A-71791
; Sequence 71791, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITPA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71791
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
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```

US-10-282-122A-71791

Query Match      59.9%; Score 238; DB 4; Length 77;
Best Local Similarity 67.1%; Pred. No. 3.8e-18;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTLERVTKIIVRLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAEK 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 2 ENPDKVKDIIVRLGVDAVDKVTEDASFKDLDGADSLDIAEVLVMELEDFGTETIPDEBAEK 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 IATVGDAVNYION 79
    | | | | | | | | | | :
DB 62 INTVGDAVKYINS 74

RESULT 11
US-10-724-972A-5601
; Sequence 5601, Application US/10724972A
; Publication No. US2004014734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 5601
; LENGTH: 79
; TYPE: PRT
; ORGANISM: S.epidermidis
US-10-724-972A-5601

Query Match      59.9%; Score 238; DB 4; Length 79;
Best Local Similarity 67.1%; Pred. No. 4e-18;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTLERVTKIIVRLGVDAVDKLEASFKEDLGADSLDVVELVMELEDFDMEISDEDAEK 66
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 ENPDKVKDIIVRLGVDAVDKVTEDASFKDLDGADSLDIAEVLVMELEDFGTETIPDEBAEK 63
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 IATVGDAVNYION 79
    | | | | | | | | | | :
DB 64 INTVGDAVKYINS 76

RESULT 12
US-10-282-122A-51523
; Sequence 51523, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
```

```
FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 51523
; LENGTH: 77
; TYPE: PR
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51523
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```
Query Match          59.4%; Score 236; DB 4; Length 77;
Best Local Similarity 60.9%; Pred. No. 6.3e-18;
Matches 42; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
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Qy      10 ERYTKIIVRLGVADVDKLEASFKEDLGADSLDVVELVMELEDFDWEISDEDAEK 69
Db      4 ERVKIINADQIGDAIEIGESSFIDDLGADSLDIIVELVMALEERDIMPDEBAEKSS 63
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Qy      70 VGDVAVNYIQ 78
Db      64 VGDVAVNYIK 72
```

```
RESULT 13
US-09-815-242-12802
; Sequence 12802, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
```

```
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12802
; LENGTH: 77
; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-815-242-12802
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Query Match          58.9%; Score 234; DB 3; Length 77;
Best Local Similarity 65.8%; Pred. No. 1e-17;
Matches 48; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
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```
Qy      7 DLEERVTKIIVRLGVADVDKLEASFKEDLGADSLDVVELVMELEDFDWEISDEDAEK 66
Db      2 ENFDKVKDIIVRLGVADKVTEDASFKDGLGADSLDIIVELVMELEDFEFTGTEIPDEBAEK 61
```

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Qy      67 IATVGDVAVNYIQ 79
Db      62 INTVGDVAVKFIN 74
```

```
RESULT 14
US-09-815-242-13101
; Sequence 13101, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13101
; LENGTH: 77
; TYPE: PR
; ORGANISM: Staphylococcus aureus
US-09-815-242-13101
```

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Query Match          58.9%; Score 234; DB 3; Length 77;
Best Local Similarity 65.8%; Pred. No. 1e-17;
Matches 48; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
```

```
Qy      7 DLEERVTKIIVRLGVADVDKLEASFKEDLGADSLDVVELVMELEDFDWEISDEDAEK 66
Db      2 ENFDKVKDIIVRLGVADKVTEDASFKDGLGADSLDIIVELVMELEDFEFTGTEIPDEBAEK 61
```

```
QY      67 IATVGDAVN YIQN 79
        | | | | | : | :
Db      62 INTVGDAVK FINS 74
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RESULT 15
116-10-293

```

US-10-282-122A-44414
/ Sequence 44414, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282.122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 44414
/ LENGTH: 77
/ TYPE: prt
/ ORGANISM: Staphylococcus aureus
US-10-282-122A-44414

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Query Match	58.9%;	Score 234;	DB 4;	Length 77;
Best Local Similarity	65.8%;	Pred. NO. 1e-17;		
Matches	48;	Conservative	9;	Mismatches 16;
				Indels 0;
				Gaps 0;

[illegible]

Search completed: December 21, 2005, 14:13:31
Job time : 90.8657 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:49, Search time 26.597 Seconds
(without alignments)
251.785 Million cell updates/sec

Title: US-10-717-138-1

Perfect score: 397

Sequence: 1 GLGSGADTLERVTIKIIVDL.....EDAEKATVGDVAVNYIQNQ 81

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/6.COMB.rep:*
- 3: /cgn2_6/prodata/1/iaa/H.COMB.rep:*
- 4: /cgn2_6/prodata/1/iaa/PCTUS.COMB.rep:*
- 5: /cgn2_6/prodata/1/iaa/R.COMB.rep:*
- 6: /cgn2_6/prodata/1/iaa/backfile1.rep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	100.0	81	2	US-09-770-834-1
2	397	59.9	79	2	US-09-134-001C-4809
3	234	58.9	77	2	US-10-089-019-26
4	225	56.7	94	2	US-09-543-681A-7956
5	222.5	56.0	80	2	US-09-902-540-14560
6	215	54.2	77	2	US-09-770-834-15
7	215	54.2	78	2	US-10-089-019-34
8	215	54.2	108	2	US-09-489-039A-7550
9	214	53.9	81	2	US-09-252-991A-18646
10	205	51.6	372	2	US-09-252-991A-30132
11	197	49.6	79	2	US-09-198-452A-308
12	197	49.6	80	2	US-09-438-185A-297
13	188	47.4	99	2	US-09-328-352-4659
14	180	45.3	86	2	US-09-107-532A-7143
15	170	42.8	111	2	US-09-248-796A-17438
16	164.5	41.4	100	2	US-09-902-540-13542
17	160	40.3	101	2	US-09-107-532A-7092
18	158.5	39.9	74	2	US-09-583-110-3914
19	158.5	39.9	74	2	US-10-089-019-30
20	154	38.8	122	2	US-09-248-796A-17437
21	153.5	38.7	77	2	US-09-383-110-4176
22	153.5	38.7	84	2	US-09-107-453-4377
23	148.5	37.4	77	2	US-08-858-207A-302
24	148.5	37.4	77	2	US-10-089-019-28
25	134	33.8	97	2	US-09-602-787A-36
26	134	33.8	97	2	US-09-852-137-2
27	122	30.7	120	2	US-09-056-556-195

28	122	30.7	120	2	US-09-072-596-190	Sequence 190, App
29	122	30.7	120	2	US-09-072-967-195	Sequence 195, App
30	122	30.7	120	2	US-10-193-002-190	Sequence 190, App
31	122	30.7	120	2	US-10-084-843-195	Sequence 195, App
32	106	26.7	136	2	US-08-580-545B-8	Sequence 8, Appli
33	106	26.7	136	2	US-09-262-653A-8	Sequence 8, Appli
34	99.5	25.1	2756	1	US-08-375-709-11	Sequence 11, Appl
35	99.5	25.1	2756	1	US-08-752-929-11	Sequence 11, Appl
36	99.5	25.1	2756	2	US-09-090-793-7	Sequence 7, Appli
37	99.5	25.1	2756	2	US-09-231-899-7	Sequence 7, Appli
38	97	24.4	41	1	US-08-453-924-8	Sequence 8, Appli
39	94	23.7	110	2	US-09-543-681A-6806	Sequence 6806, Ap
40	93.5	23.6	93	2	US-09-266-965-117	Sequence 117, App
41	91.5	23.0	1481	2	US-09-231-899-70	Sequence 117, App
42	85.5	21.5	85	2	US-09-902-540-13340	Sequence 13340, A
43	84	21.2	40	1	US-08-129-129-6	Sequence 6, Appli
44	83	20.9	359	2	US-09-266-965-120	Sequence 120, App
45	76	19.1	84	1	US-08-901-306-4	Sequence 4, Appli

ALIGNMENTS

```
RESULT 1
US-09-770-834-1
Sequence 1, Appli
Patent No. 6684162
GENERAL INFORMATION:
APPLICANT: Patris, Kevin
APPLICANT: Somers, William
APPLICANT: Tam, Amy
APPLICANT: Lin, Laura
APPLICANT: Stahl, Mark
APPLICANT: Powers, Robert
APPLICANT: Xu, Guan-Yi
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPs/ACP COMPLEX, SOLUTION STRUCTURE
TITLE OF INVENTION: OF B. SUBSTITIS ACP, AND USES THEREOF
FILE REFERENCE: 2368/14
CURRENT APPLICATION NUMBER: US/09/770,834
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 81
TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-770-834-1
Query Match 100.0%; Score 397; DB 2; Length 81;
Best local similarity 100.0%; Pred. No. 2.8e-40;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLGSGADTLERVTIKIIVDLGVDEADVKKLEAFKEDIGADSIDVVELVMELEDFEPMETS 60
DB 1 GLGSGADTLERVTIKIIVDLGVDEADVKKLEAFKEDIGADSIDVVELVMELEDFEPMETS 60
QY 61 DEDAEKATVGDVAVNYIQNQ 81
DB 61 DEDAEKATVGDVAVNYIQNQ 81
RESULT 2
US-09-134-001C-4809
Sequence 4809, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
```

```

; APPLICANT: XU, Guan-Yi
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF ACPS/ACP COMPLEX, SOLUTION STRUCTURE
; TITLE OF INVENTION: OF B. SUBTILIS ACP, AND USES THEREOF
; FILE REFERENCE: 2368/14

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CURRENT APPLICATION NUMBER: US/09/770,834
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/202,466
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
LENGTH: 77
TYPE: PRF
ORGANISM: Escherichia coli
US-09-770-834-15

Query Match 54.2%; Score 215; DB 2; Length 77;
Best Local Similarity 63.9%; Pred. No. 1.7e-18;
Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 10 ERYTKIIVRLGVDEADVLEASFKEDELGADSLDVLVMELEDEPFDEMSDEDAKTIAT 69
DB 5 ERYVKTIIGSQLGVKEEVNTNNSFVEDLGADSLDVLVMELEDEPFDEMSDEDAKTIAT 64

QY 70 VGDVAVYIQNOQ 81
DB 65 VQAADIDYINGHQ 76

RESULT 7
US-10-089-019-34
Sequence 34, Application US/10089019
Patent No. 6951729
GENERAL INFORMATION:
APPLICANT: DEMOLF, WALTER E. JR
APPLICANT: KALENDER, HOWARD
APPLICANT: LONSDALE, JOHN T.
TITLE OF INVENTION: METHODS FOR MAKING AND USING FATY ACID
TITLE OF INVENTION: SYNTHESIS PATHWAY REAGENTS
FILE REFERENCE: GMS50068
CURRENT APPLICATION NUMBER: US/10/089,019
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: PCT/US00/29451
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/161,775
PRIOR FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 78
TYPE: PRF
ORGANISM: Escherichia coli
US-10-089-019-34

Query Match 54.2%; Score 215; DB 2; Length 78;
Best Local Similarity 63.9%; Pred. No. 1.7e-18;
Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 10 ERYTKIIVRLGVDEADVLEASFKEDELGADSLDVLVMELEDEPFDEMSDEDAKTIAT 69
DB 6 ERYVKTIIGSQLGVKEEVNTNNSFVEDLGADSLDVLVMELEDEPFDEMSDEDAKTIAT 65

QY 70 VGDVAVYIQNOQ 81
DB 66 VQAADIDYINGHQ 77

RESULT 8
US-09-489-039A-7550
Sequence 7550, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7550
LENGTH: 108
TYPE: PRF
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7550

Query Match 54.2%; Score 215; DB 2; Length 108;
Best Local Similarity 63.9%; Pred. No. 2.7e-18;
Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 10 ERYTKIIVRLGVDEADVLEASFKEDELGADSLDVLVMELEDEPFDEMSDEDAKTIAT 69
DB 36 ERYVKTIIGSQLGVKEEVNTNNSFVEDLGADSLDVLVMELEDEPFDEMSDEDAKTIAT 95

QY 70 VGDVAVYIQNOQ 81
DB 96 VQAADIDYINGHQ 107

RESULT 9
US-09-252-991A-18646
Sequence 18646, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18646
LENGTH: 81
TYPE: PRF
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18646

Query Match 53.9%; Score 214; DB 2; Length 81;
Best Local Similarity 59.0%; Pred. No. 2.4e-18;
Matches 46; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 4 GSADTLERYTKIIVRLGVDEADVLEASFKEDELGADSLDVLVMELEDEPFDEMSDEDAKTIAT 63
DB 3 GMSITTEERYTKIIVRLGVDEADVLEASFKEDELGADSLDVLVMELEDEPFDEMSDEDAKTIAT 62

QY 64 AEKIAVGDVAVYIQNOQ 81
DB 63 AEKITTVEAIDYINGHQ 80

RESULT 10
US-09-252-991A-30132
Sequence 30132, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30132
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30132

Query Match 51.6%; Score 205; DB 2; Length 372;
Best Local Similarity 50.0%; Pred. No. 2.2e-16;
Matches 39; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 1 GPLGSADTERTYKIIIVDRIGVDEADVLEKLEASFKEDIGADSLDVLELVMELEDFPMEIS 60
DB 290 GQGCNDIDITRKVLVAALFGEBCIRLSDSPRDFGALSLEVELVWALFAEFGEVLA 349

QY 61 DEDAEKIATVGDAVNYIQ 78
DB 350 DDAERIEFTVROAIDYLE 367

RESULT 11
US-09-198-452A-308
; Sequence 308, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:

APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 308
LENGTH: 79
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-308

Query Match 49.6%; Score 197; DB 2; Length 79;
Best Local Similarity 57.1%; Pred. No. 2.5e-16;
Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 12 VKKIIVDRIGVDEADVLEKLEASFKEDIGADSLDVLELVMELEDFPMEISDEDAEKIATVG 71
DB 7 VIAIIVGQGVDPKEVENSFFIEDLNADSLDTLITLTKFAFELISEDAEKIATVG 66

QY 72 DAVNYIONQO 81
DB 67 DVFTYIKKRQ 76

RESULT 12
US-09-438-185A-297
; Sequence 297, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kaiman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 297

LENGTH: 80
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: Cpn0295
US-09-438-185A-297

Query Match 49.6%; Score 197; DB 2; Length 80;
Best Local Similarity 57.1%; Pred. No. 2.6e-16;
Matches 40; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 12 VKKIIVDRIGVDEADVLEKLEASFKEDIGADSLDVLELVMELEDFPMEISDEDAEKIATVG 71
DB 8 VIAIIVGQGVDPKEVENSFFIEDLNADSLDTLITLTKFAFELISEDAEKIATVG 67

QY 72 DAVNYIONQO 81
DB 68 DVFTYIKKRQ 77

RESULT 13
US-09-328-352-4669
; Sequence 4669, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4669
LENGTH: 99
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4669

Query Match 47.4%; Score 188; DB 2; Length 99;
Best Local Similarity 48.6%; Pred. No. 4.1e-15;
Matches 35; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 6 ADTLERVTKIIVDRIGVDEADVLEKLEASFKEDIGADSLDVLELVMELEDFPMEISDEDAE 65
DB 23 SDIERGVQAAVEQGLKAERIKNEASFMDDLGADSLDVLELVWVSNFENDPITIPDESN 82

QY 66 KIATVGDAVNYI 77
DB 83 EITTVQSAIDVY 94

RESULT 14
US-09-107-532A-7143
; Sequence 7143, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
APPLICANT: Lynn A. Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESS: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:41:34 ; Search time 118.075 Seconds
(without alignments)
483.997 Million cell updates/sec

Title: US-10-717-138-1
Perfect score: 397
Sequence: 1 GPLGSADTLRLVTKIIVDL.....EDAEKIAIVGDAVNTIQNQ 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_05.86:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	37.0	93.2	77	1	ACP_BACSU	P80643 bacillus su
2	34.5	86.9	77	2	Q65706_BACLD	Q65706 bacillus li
3	31.5	79.3	77	2	Q51004_GEOXA	Q51004 geobacillus
4	31.3	78.8	77	1	ACP_BACSD	Q9ka04 bacillus ha
5	31.1	78.3	77	1	ACP_BACSK	Q5wf55 bacillus cl
6	30.2	76.1	77	1	ACP_BACSN	Q81w17 bacillus an
7	30.2	76.1	77	1	ACP_BACCL	Q732a0 bacillus ce
8	30.2	76.1	77	1	ACP_BACCR	Q819v7 bacillus ce
9	30.2	76.1	77	1	ACP_BACCC	Q636b6 bacillus ce
10	30.2	76.1	77	1	ACP_BACCH	Q6hew5 bacillus th
11	30.2	76.1	77	2	Q4MH03_BACEE	Q4mh03 bacillus ce
12	28.4	71.5	77	1	ACP_LISIN	P63440 listeria in
13	28.4	71.5	77	1	ACP_LISMF	Q71y10 listeria mo
14	28.4	71.5	77	1	ACP_LISMO	P63439 listeria mo
15	27.1	68.3	77	1	ACP_OCEIH	Q8er06 oceanobacil
16	25.4	64.0	76	1	ACP_HAEIN	P43709 haemophilus
17	25.4	64.0	76	1	ACP_MANEM	Q65rc8 manheimia
18	25.4	64.0	76	2	Q4QF33_HABE8	Q4qf33 haemophilus
19	24.9	62.7	76	1	ACP_PASRU	Q9c3j5 pasteurella
20	24.9	62.7	76	1	Q67PF6_SYMRH	Q67pf6 pasteurella
21	24.7	62.2	77	2	Q4VK22_VIBAN	Q4vk22 vibrio angu
22	24.4	61.5	76	1	ACP_VIBHA	P0a2w3 vibrio harv
23	24.4	61.5	76	1	ACP_VIBBA	P0a2w2 vibrio para
24	24.3	61.2	77	2	Q5E112_VIBF1	Q5e112 vibrio fisc
25	23.9	60.2	77	1	ACP_VIBCH	Q9kq48 vibrio chol
26	23.8	59.9	77	1	ACP_STAEP	Q8cp12 staphylococ
27	23.8	59.9	77	2	Q4L574_STAHJ	Q4l574 staphylococ
28	23.8	59.9	77	2	Q5HPV9_STAEO	Q5hpv9 staphylococ
29	23.6	59.4	77	1	ACP_CLOAB	Q7h155 clostridium
30	23.6	59.4	77	1	ACP_VIBVY	Q8d869 vibrio vuln
31	23.6	59.4	78	1	ACP_VIBVY	Q7m129 vibrio vuln

32	23.5	59.2	77	1	ACP_HAEUD	Q7vk6 haemophilus
33	23.4	58.9	77	1	ACP_STAAM	P0a001 staphylococ
34	23.4	58.9	77	1	ACP_STAAN	P0a002 staphylococ
35	23.4	58.9	77	1	ACP_STAAR	Q6ghk3 staphylococ
36	23.4	58.9	77	1	ACP_STAAS	Q6g9y1 staphylococ
37	23.4	58.9	77	1	ACP_STAAN	P0a003 staphylococ
38	23.4	58.9	77	2	Q5HGK0_STPAC	Q5hgk0 staphylococ
39	23.3	58.7	76	1	ACP_THETN	Q8x9w1 thermococ
40	23.3	58.7	78	2	Q7N387_PHOHL	Q7n387 photorhabd
41	23.2	58.4	78	1	ACP_PHOFR	Q9r6z3 photobacter
42	23.1	58.2	79	2	Q5QZ29_IDITLO	Q5qz29 idiomarina
43	23.0	57.9	77	1	ACP_GEOSL	Q7ac8 geobacter s
44	23.0	57.9	77	1	ACP_LEPIC	Q75fw6 leptospira
45	23.0	57.9	77	1	ACP_LEPIN	Q8exx4 leptospira

ALIGNMENTS

RESULT 1	ACP_BACSU	STANDARD:	PRT:	77 AA.
AC	P80643; P51832;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Acyl carrier protein (ACP)			
GN	Name=acpa; Synonyms=acp; Ordered locus Names=BSU15920;			
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1423;			
RN	[1]			
RP	PROTEIN SEQUENCE OF 15-77, AND NUCLEOTIDE SEQUENCE OF 1-14.			
RC	STRAIN=168;			
RX	MEDLINE=96326321; PubMed=8759840;			
RA	Morbidoni H.R., de Mendoza D., Cronan J.E. Jr.;			
RT	"Bacillus subtilis acyl carrier protein is encoded in a cluster of			
RT	lipid biosynthesis genes";			
RT	J. Bacteriol. 178:4794-4800(1996).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=168;			
RX	MEDLINE=96257247; PubMed=8654983; DOI=10.1016/0378-1119(96)00181-3;			
RA	Kunet F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,			
RA	Azevedo V., Bertoletti M., Bessieres P., Bolotin A., Borchert S.,			
RA	Borisov R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,			
RA	Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,			
RA	Choi S.-K., Codani U.-J., Cornerton I.F., Cummings N.J., Daniel R.A.,			
RA	Denicot F., Devane K.M., Duesterhoeft A., Ehlich S.D., Emmerson P.T.,			
RA	Enlison K.-D., Etrington J., Fabret C., Ferrari E., Foulger D.,			
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,			
RA	Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,			
RA	Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,			
RA	Hilbert H., Holtsappel S., Hosono S., Hullo M.-F., Itaya M.,			
RA	Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaer-Bianchard M.,			
RA	Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,			
RA	Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,			
RA	Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,			
RA	Medine C., Meene D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,			
RA	Noback M., Nore D., Pohl T.M., Portecelle D., Porrolik S.,			
RA	Park S.-H., Patro V., Pohl T.M., Portecelle D., Porrolik S.,			
RA	Prescott A.M., Presseau E., Pujic P., Purnelle B., Rapoport G.,			
RA	Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,			
RA	Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R.,			
RA	Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P.,			

RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terasaka P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
 RA Vassarotti A., Viari A., Wandut R., Wedler E., Wedler H.,
 RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zimstein E.,
 RA Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.";
 RT Nature 390:249-256(1997).
 RN [4]
 RN PROTEIN SEQUENCE OF 1-17.
 RP MEDLINE=94131947; PubMed=8300523;
 RX Heaton M.P., Neuhaus F.C.;
 RA "Role of the D-alanyl carrier protein in the biosynthesis of D-alanyl-lipoteichoic acid.";
 RT J. Bacteriol. 176:681-690(1994).
 RL [5]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF HOLO-(ACYL CARRIER PROTEIN)
 RP IN COMPLEX WITH HOLO-(ACYL CARRIER PROTEIN) SYNTHASE.
 RX PubMed=10997907; DOI=10.1016/S0969-2126(00)00178-7
 RA Parais K.D., Lin L., Tam A., Mathew R., Hixon J., Stahl M.,
 RA Fritz C.C., Seehra J., Somers W.S.;
 RT "Crystal structures of substrate binding to *Bacillus subtilis* holo-(acyl carrier protein) synthase reveal a novel trimeric arrangement of molecules resulting in three active sites.";
 RT Structure 8:883-895(2000).
 RN [6]
 RN STRUCTURE BY NMR.
 RX MEDLINE=21416009; PubMed=11525165; DOI=10.1016/S0969-2126(01)00586-X;
 RA Xu G.-Y., Tam A., Lin L., Hixon J., Fritz C.C., Powers R.;
 RT "Solution structure of *B. subtilis* acyl carrier protein.";
 RL Structure 9:277-287(2001).
 CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid biosynthesis.
 CC -1- PATHWAY: De novo fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific serine of apo-ACP by acps. This modification is essential for activity because fatty acids are bound in thioester linkage to the sulphydryl of the prosthetic group.
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 DR EMBL, U59433; AAC4308.1; -; Genomic DNA.
 DR EMBL, D64116; BA010975.1; -; Genomic DNA.
 DR EMBL, Z59112; CAB13465.1; -; Genomic DNA.
 DR PIR, JC4822; JC4822.
 DR PIR, T46634; T46634.
 DR PDB, 1F80; X-ray; D/E/F=-.
 DR PDB, 1Y80; NMR; A=2-77.
 DR Subtilist, BG1536; acpa.
 DR HAMAP, MF_01217; -; 1.
 DR InterPro, IPR009081; ACP_1like.
 DR InterPro, IPR003231; Acyl carrier.
 DR InterPro, IPR006163; Phosphopantetheine_bd.
 DR InterPro, IPR006162; Pantane_S.
 DR Pfam, PF00550; PP-binding; 1.
 DR Pfam, PD000887; Acyl_carrier; 1.
 DR TIGRfam, TIGR00517; acyl_carrier; 1.
 DR PROSITE, PS50075; ACP DOMAIN; 1.
 DR PROSITE, PS50012; PHOSPHOPANTHEINE; 1.
 KW 3D-structure; Complete proteome; Direct protein sequencing; Fatty acid biosynthesis; Lipid synthesis; Phosphopantetheine.
 FT BINDING 37 37 Phosphopantetheine (covalent).
 FT HELIX 3 16
 FT TURN 25 26
 FT STRAND 28 28

FT HELIX 29 33
 FT HELIX 37 50
 FT TURN 51 52
 FT HELIX 57 61
 FT TURN 62 62
 FT STRAND 65 65
 FT HELIX 66 74
 SQ SEQUENCE 77 AA; 8591 MW; 75E745DE3C6A0951 CRC64;
 Query Match 93.2%; Score 370; DB 1; Length 77;
 Best Local Similarity 100.0%; Pred. No. 6.1e-24;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 ADTERVTKIVDPDGVDEADVKLEASFKEDLGADSLVVELVMELEDEDFMEISDDAE 65
 DB 2 ADTERVTKIVDPDGVDEADVKLEASFKEDLGADSLVVELVMELEDEDFMEISDDAE 61
 QY 66 KIATVGDAVNYIQNQ 81
 DB 62 KIATVGDAVNYIQNQ 77
 RESULT 2
 ID Q65J06 BACLD PRELIMINARY; PRT; 77 AA.
 AC Q65J06; Q62V61;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE ACPa (acyl carrier protein).
 OS Name=acpa; OrderedLocName=BL02316, BL101813;
 OS *Bacillus licheniformis* (strain DSM 316 / ATCC 14580).
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 OX NCBI_Taxid=279010;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=15461803; DOI=10.1159/000079829;
 RA Velt B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
 RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,
 RA Ehrenreich A., Gottschalk G.;
 RT "The complete genome sequence of *Bacillus licheniformis* DSM13, an organism with great industrial potential.";
 RT J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RP PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;
 RA Rey M.W., Kameiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., Lopez de Leon A., Xiang H., Gueti V., Clausen I.G.,
 RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
 RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
 RA Ehrlich S.D., Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium *Bacillus licheniformis* and comparisons with closely related *Bacillus* species.";
 RT Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.
 DR EMBL, AE017333; AAU40708.1; -; Genomic DNA.
 DR EMBL, CP000002; AAU23348.1; -; Genomic DNA.
 DR SMR, Q65J06; 2-77.
 DR GO, GO:0000036; F:acyl carrier activity; IEA.
 DR GO, GO:0048037; F:cofactor binding; IEA.
 DR GO, GO:0031177; F:phosphopantetheine binding; IEA.
 DR GO, GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro, IPR009081; ACP_1like.
 DR InterPro, IPR003231; Acyl_carrier.
 DR InterPro, IPR006163; Phosphopantetheine_bd.
 DR InterPro, IPR006162; Pantane_S.
 DR Pfam, PF00550; PP-binding; 1.
 DR Pfam, PD000887; Acyl_carrier; 1.
 DR TIGRfam, TIGR00517; acyl_carrier; 1.
 DR PROSITE, PS50075; ACP DOMAIN; 1.
 DR PROSITE, PS50012; PHOSPHOPANTHEINE; 1.
 KW Complete proteome; Phosphopantetheine.
 SQ SEQUENCE 77 AA; 8493 MW; 9AFDA53DB6C6C033C CRC64;

Query Match 86.9%; Score 345; DB 2; Length 77;
 Best Local Similarity 93.4%; Pred. No. 86-22;
 Matches 71; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 ADLTERVTKIIVDRGLGVDAVDKLEASFKEDLGADSLDVVLELMEDEPFDMETISDEDAE 65
 DB 2 ADLTERVTKIIVDRGLGVDAVDKLEASFKEDLGADSLDVVLELMEDEPFDMETISDEDAE 61
 QY 66 KIATVGDAVNYIIONQ 81
 DB 62 KIATVGDAVNYIIONQ 77

RESULT 3
 OS1004_GEOKA PRELIMINARY; PRT; 77 AA.

AC OS1004; 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Acyl carrier protein (ACP).
 GN OrderedLocuNames=GK1191;
 OS Geobacillus kaustophilus;
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1462;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HTM426;
 RX PubMed=1576355; DOI=10.1093/nar/gkh970;
 RA Takami H., Takaki Y., Chee G.-Y., Nishi S., Shimamura S., Suzuki H.,
 RT Matsui S., Uchiyama I.;
 RT "Thermoadaptation trait revealed by the genome sequence of
 RT thermophilic Geobacillus kaustophilus";
 RL Nucleic Acids Res. 32:6292-6303(2004).
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.
 CC EMBL; BA000043; BAD75476.1; -; Genomic_DNA.
 DR SMR; OS1004; 2-76.
 DR GO; GO:0000036; F:acyl carrier activity; IEA.
 DR GO; GO:0048037; F:cofactor binding; IEA.
 DR GO; GO:0031177; F:phosphopantetheine binding; IEA.
 DR GO; GO:0006633; F:fatty acid biosynthesis; IEA.
 DR GO; GO:0006633; F:fatty acid biosynthesis; IEA.
 DR InterPro; IPR006163; Phosphateth_bind.
 DR InterPro; IPR006162; Pantane_S.
 DR Pfam; PF00550; PP-binding_1
 DR ProDom; PD000867; Acyl_carrier; 1.
 DR TIGRfam; TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS50075; ACP DOMAIN; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 KW Complete proteome; Phosphopantetheine.
 SQ SEQUENCE 77 AA; 8619 MW; C47CC6C7BCF4BA4C CRC64;

Query Match 79.3%; Score 315; DB 2; Length 77;
 Best Local Similarity 84.0%; Pred. No. 2-76-19;
 Matches 63; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 6 ADLTERVTKIIVDRGLGVDAVDKLEASFKEDLGADSLDVVLELMEDEPFDMETISDEDAE 65
 DB 2 ADLTERVTKIIVDRGLGVDAVDKLEASFKEDLGADSLDVVLELMEDEPFDMETISDEDAE 61
 QY 66 KIATVGDAVNYIIONQ 80
 DB 62 KIATVGDAVNYIIONQ 76

RESULT 4
 ACP_BACHD STANDARD; PRT; 77 AA.
 AC OSKAO4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Acyl carrier protein (ACP).
 GN Name=acpP; Synonyms=acpA; OrderedLocuNames=BH2490;
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sesaki R., Masui N.,
 RA Fuji F., Hirama C., Nakamura Y., Ogatawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
 CC biosynthesis (By similarity).
 CC -1- PATHWAY: De novo fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
 CC serine of apo-ACP by acpS. This modification is essential for
 CC activity because fatty acids are bound in thioester linkage to the
 CC sulfhydryl of the prosthetic group (By similarity).
 CC -1- SIMILARITY: Contains 1 acyl carrier domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; BA000004; BAB06209.1; -; Genomic_DNA.
 DR PIR; B83961; B83961.
 DR HSSP; P80643; IHY8.
 DR SMR; OSKAO4; 2-77.
 DR HAMAP; MF_01217; -; 1.
 DR InterPro; IPR009081; ACP_like.
 DR InterPro; IPR003221; Acyl_carrier.
 DR InterPro; IPR006163; Phosphateth_bd.
 DR InterPro; IPR006162; Pantane_S.
 DR Pfam; PF00550; PP-binding_1.
 DR ProDom; PD000867; Acyl_carrier; 1.
 DR TIGRfam; TIGR00517; acyl_carrier; 1.
 DR PROSITE; PS50075; ACP DOMAIN; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
 KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
 KW Phosphopantetheine.
 FT BINDING 37 Phosphopantetheine (covalent) (By
 FT similarity).
 SQ SEQUENCE 77 AA; 8558 MW; 3575CDFA5BA15CA CRC64;

Query Match 78.8%; Score 313; DB 1; Length 77;
 Best Local Similarity 81.6%; Pred. No. 4e-19;
 Matches 62; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 6 ADLTERVTKIIVDRGLGVDAVDKLEASFKEDLGADSLDVVLELMEDEPFDMETISDEDAE 65
 DB 2 ADLTERVTKIIVDRGLGVDAVDKLEASFKEDLGADSLDVVLELMEDEPFDMETISDEDAE 61
 QY 66 KIATVGDAVNYIIONQ 81
 DB 62 KIATVGDAVNYIIONQ 77

RESULT 5
 ACP_BACSK STANDARD; PRT; 77 AA.
 AC OSWFM5;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Acyl carrier protein (ACP).
 GN Name=acpP; Synonyms=acpA; OrderedLocuNames=ABC3300;

Query Match	Best Local Similarity	Matches	Score	DB	Length	Pred.	No. gaps	Indels	Gaps	Indels
6 ADTLERKTIIVDRIGDEADVVKLEASKEKDLGADSLVVELVWELREDFPMETISDEDAE	78.3%	63	311	DB 1	77	66	0	0	0	0
2 ADVERRVTKIIIVDRIGVESEKVESSEKEDLKADSLVVELVWELREDFMETIADDEAE	82.9%	7	66	19	77	62	0	0	0	0
66 KIATGVADVANYTIONQO	81	62	62	62	62	62	0	0	0	0
62 KIATVKDYYVDIINNNO	77	62	62	62	62	62	0	0	0	0

RA	MEBLIN=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA	Read T.D., Peterson S.N., Tounasse N.J., Baillie L.W., Paulsen I.T.,
RA	Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA	Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA	Koloney J.F., Benam M.J., Dodson R.J., Brinkac L.M., Gwyn M.L.,
RA	DeJoy R.T., Madry R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA	Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radue D.,
RA	Berry J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA	Berry K.J., Plant R.D., Wolf A.M., Watkins K.L., Niemman W.C.,
RA	Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA	Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
RA	Hanna P.C., Kolstoe A.-B., Fraser C.M.,
RT	"The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to
RT	closely related bacteria."
RL	Nature 423:81-86(2003).
RL	[2]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP	STRAIN=Ames / isolate 0581;
RC	Ravel J., Raso D.A., Shumway M.F., Jiang L., Cer R.-Z., Federova N.B.,
RA	Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA	Fraser C.M.,
RT	" <i>Bacillus anthracis</i> comparative genomes."
RL	Submitted (May-2004) to the EMBL/Genbank/DBJ databases.
RN	[3]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	STRAIN=Stearne;
RA	Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA	Hitchcock P., Jackson P., Kelm P., Longmire J., Lucas S., Okitaka R.,
RA	Richardson P., Rubin E., Tice H.,
RT	"Complete genome sequence of <i>Bacillus anthracis</i> Stearne."
RL	Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
CC	-1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC	biosynthesis (By similarity)
CC	-1- PATHWAY: De novo fatty acid biosynthesis.
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC	-1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC	serine of apo-ACP by acps. This modification is essential for
CC	activity because fatty acids are bound in thioester linkage to the
CC	sulphydryl of the prosthetic group (By similarity).
CC	-1- SIMILARITY: Contains 1 acyl carrier domain.
CC	-----
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
CC	-----
CC	EMBL, AE017036; AAP27716.1; -; Genomic DNA.
CC	EMBL, AE017334; AAT33103.1; -; Genomic DNA.
CC	EMBL, AE017225; AAT56003.1; -; Genomic DNA.
DR	HSSP, P80643; IFS0.
DR	SMR, Q81W17; 2-76.
DR	TIGR, BA3988; -.
DR	TIGR, GBA3988; -.
DR	HAMAP, MF_01217; -; 1.
DR	InterPro, IPR009081; ACP_like
DR	InterPro, IPR003231; ACP_carrier.
DR	InterPro, IPR006163; Phosphopanteth_bd.
DR	InterPro, IPR006162; Pantne S_
DR	Pfam, PF00500; pp-binding; 1.
DR	ProDom, P000987; ACP_carrier; 1.
DR	TIGRFAMs, TIGR00517; acyl_carrier; 1.
DR	PROSITE, PS50075; ACP_DOMAIN; 1.
DR	PROSITE, PS00012; PHOSPHOPANTETHEINE; 1.
KW	Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
FT	Phosphopantetheine.
FT	BINDING 37 37 Phosphopantetheine (covalent) (By
FT	similarity).
FT	SEQUENCE 77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;
Query Match	76.1%; Score 302; DB 1; Length 77;
Best Local Similarity	83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative	6; Mismatches 6; Indels 0; Gaps 0.

```

QY 6 ADTLERVTKIIVRLGVDEADVKTLEASFKEIDLGADSLDVVELVMELEDFEPMESIDEDAE 65
DB 2 ADVLERVTKIIVRLGVDEADVKTLEASFKEIDLGADSLDVVELVMELEDFEPMESIDEDAE 61
QY 66 KIATVGDADVNTION 79
DB 62 KIATVGDADVNTIES 75

RESULT 7
ACQ_BACCI STANDARD; PRT; 77 AA.
ID ACQ_BACCI
AC 0732M0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpP; Synonyms=acpA; OrderedLocustNames=BC3892;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=225253;
ON [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Osekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tounouse N.J., Angiolini S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1."
RL Nucleic Acids Res. 32:977-988(2004).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
CC
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CC removed.
CC
CC -----
CC EMBL; AE017276; AAS42797.1; -; Genomic_DNA.
CC HSSP; P02901; IACP.
CC SMR; Q732M0; 2-76.
CC TIGR; BCE3892; -.
CC HAMAP; MF_01217; -; 1.
CC InterPro; IPR009081; ACP like.
CC InterPro; IPR003231; Acyl carrier.
CC InterPro; IPR006163; Phosphopanteth_bd.
CC InterPro; IPR006162; Ppantne_S.
CC Pfam; PF00550; PP-binding; 1.
CC ProDom; PD000887; Acyl carrier; 1.
CC TIGRFAMs; TIGR00517; acyl carrier; 1.
CC TIGRFAMs; TIGR00517; acyl carrier; 1.
CC PROSITE; PS00075; ACP DOMAIN; 1.
CC PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
FT BINDING 37 Phosphopantetheine (covalent) (By
FT similarity).
SQ SEQUENCE 77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;
Query Match 76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 6 ADTLERVTKIIVRLGVDEADVKTLEASFKEIDLGADSLDVVELVMELEDFEPMESIDEDAE 65

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DB 2 ADVLERVTKIIVRLGVDEADVKTLEASFKEIDLGADSLDVVELVMELEDFEPMESIDEDAE 61
QY 66 KIATVGDADVNTION 79
DB 62 KIATVGDADVNTIES 75

RESULT 8
ACQ_BACCR STANDARD; PRT; 77 AA.
ID ACQ_BACCR
AC 0819V7;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpP; OrderedLocustNames=BC3848;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
ON [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RX Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldsman E., Larsen N., P'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fomstein M., Ehrlich S.D.,
RA Overbeek R., Kyriades N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
CC
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CC
CC -----
CC EMBL; AE017010; AAP10770.1; ALT_INIT; Genomic_DNA.
CC HSSP; P80643; 1F80.
CC SMR; Q819V7; 2-76.
CC HAMAP; MF_01217; -; 1.
CC InterPro; IPR009081; ACP like.
CC InterPro; IPR003231; Acyl carrier.
CC InterPro; IPR006163; Phosphopanteth_bd.
CC InterPro; IPR006162; Ppantne_S.
CC Pfam; PF00550; PP-binding; 1.
CC ProDom; PD000887; Acyl carrier; 1.
CC TIGRFAMs; TIGR00517; acyl carrier; 1.
CC TIGRFAMs; TIGR00517; acyl carrier; 1.
CC PROSITE; PS00075; ACP DOMAIN; 1.
CC PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
FT BINDING 37 Phosphopantetheine (covalent) (By
FT similarity).
SQ SEQUENCE 77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;
Query Match 76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 6 ADTLERVTKIIVRLGVDEADVKTLEASFKEIDLGADSLDVVELVMELEDFEPMESIDEDAE 65

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Db      2 ADLBRVTKIIVDRIGVETEVVPAASFKEIDLGDLSLVDVLELWQLEDFEFMEISDEDAE 61
QY      66 KIATVGDAVNYION 79
        |||||
Db      62 KIATVGDAVNTYES 75

RESULT 9
ACP_BACCZ STANDARD; PRT; 77 AA.
ID_ACP_BACCZ
AC Q636H6;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Acyl carrier protein (ACP)
GN Name=acpP; Synonyms=acpA; OrderedLocustNames=BCZK3609;
OS Bacillus cereus (strain ZK);
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: Contains 1 acyl carrier domain.
CC -----
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CC removed.
CC -----
DR EMBL; CP000001; AAU1654.1; -; Genomic_DNA.
DR SMR; Q636H6; 2-76.
DR HAMAP; MF_01217; -; 1.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR006163; Phosphopanteth_bd.
DR InterPro; IPR006162; Pantane S.
DR Pfam; PF00550; PP-binding; 1.
DR ProDom; PD000887; Acyl_carrier; 1.
DR TIGRFAMs; TIGR00517; acyl_carrier; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Phosphopantetheine.
FT BINDING 37 Phosphopantetheine (covalent) (By
FT similarity).
SQ SEQUENCE 77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;

Query Match 76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```

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RESULT 10
ACP_BACHK STANDARD; PRT; 77 AA.
ID_ACP_BACHK
AC Q6H5W5;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Acyl carrier protein (ACP).
GN Name=acpP; Synonyms=acpA; OrderedLocustNames=Bt9727_3591;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: Contains 1 acyl carrier domain.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE017355; AAT61346.1; -; Genomic_DNA.
DR SMR; Q6H5W5; 2-76.
DR HAMAP; MF_01217; -; 1.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR006163; Phosphopanteth_bd.
DR InterPro; IPR006162; Pantane S.
DR Pfam; PF00550; PP-binding; 1.
DR ProDom; PD000887; Acyl_carrier; 1.
DR TIGRFAMs; TIGR00517; acyl_carrier; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
KW Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
KW Phosphopantetheine.
FT BINDING 37 Phosphopantetheine (covalent) (By
FT similarity).
SQ SEQUENCE 77 AA; 8513 MW; 8CCA3CBAE5DA0AB CRC64;

Query Match 76.1%; Score 302; DB 1; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```

```

RESULT 11
Q4MH03_BACCE PRELIMINARY; PRT; 77 AA.
ID Q4MH03;
AC Q4MH03;

```

```

DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Acyl carrier protein.
GN Name=acpP; ORFNames=BCE_G9241_3833;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Baker M., Jiang L., Cer R.Z.,
RA Ralston J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax."
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -1- FUNCTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAEK0100080; EAL11450.1; -; Genomic_DNA.
CC SEQENCE 77 AA; 8513 MW; 8CCAC3CBAS5DA0AB CRC64;

Query Match 76.1%; Score 302; DB 2; Length 77;
Best Local Similarity 83.8%; Pred. No. 3.4e-18;
Matches 62; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 6 ADLTERVTKIIVDRIGVDADVLEASFKEDLGADSLDVLELWMELEDFEPMESDEDAE 65
DB 2 ADVLEKVTIKIIVDRIGVETEVVPASFKEDLGADSLDVLELWMELEDFEPMESDEDAE 61
QY 66 KIATVGDAVNYIQ 79
DB 62 KIATVGDAVNYIES 75

RESULT 12
ACP_LISIN STANDARD; PRT; 77 AA.
ID _ACP_LISIN STANDARD; PRT; 77 AA.
AC P63440; Q92AK2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpP; Synonyms=acpA; OrderedLocustNames=lin1920;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangoul L., Buchrieser C., Ruenick C., Amend A.,
RA Baquero F., Cherouat P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duesurget O.,
RA Entian K.-D., Fahl H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species."
RL Science 294:849-852(2001).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (by similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).

```

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CC -1- PPM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (by similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL596170; CAC97150.1; -; Genomic_DNA.
CC PIR; A1672; A1672.
CC HSSP; P80643; 1H78.
CC SMR; P63440; 2-74.
CC Listlist; LIND01920; -.
CC HAMAP; MF_01217; -; 1.
CC InterPro; IPR009081; ACP like.
CC InterPro; IPR003231; Acyl carrier.
CC InterPro; IPR006163; Phosphopanteth_b.
CC InterPro; IPR005162; Ppantne_S.
CC Pfam; PF00550; pp-binding; 1.
CC ProDom; PD000887; Acyl carrier; 1.
CC TIGRFAMs; TIGR00517; acyl carrier; 1.
CC PROSITE; PS00075; ACP DOMAIN; 1.
CC PROSITE; PS00012; PHOSPHOPANTHETHEINE; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
CC BINDING 37 Phosphopantetheine (covalent) (by
CC similarity);
CC FT SEQUENCE 77 AA; 8359 MW; 8DEF7E28C1F192E21 CRC64;

Query Match 71.5%; Score 284; DB 1; Length 77;
Best Local Similarity 80.8%; Pred. No. 1.1e-16;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 6 ADLTERVTKIIVDRIGVDADVLEASFKEDLGADSLDVLELWMELEDFEPMESDEDAE 65
DB 2 AEVLEKVTIKIIVDRIGVESKVLASFKEDLGADSLDVLELWMELEDFEPMESDEDAE 61
QY 66 KIATVGDAVNYIQ 78
DB 62 NINTVGDAVKIE 74

RESULT 13
ACP_LISMF STANDARD; PRT; 77 AA.
ID _ACP_LISMF STANDARD; PRT; 77 AA.
AC Q71YU0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpP; OrderedLocustNames=LMOF2365_1834;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nielsen W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Katharou S., Wonderling L.D., Unlrich G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
RT borne pathogen Listeria monocytogenes reveal new insights into the
RT core genome components of this species."
RL Nucleic Acids Res. 32:2386-2395(2004).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid

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CC biosynthesis (By similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL, AB017328; AAT04604.1; -, Genomic_DNA.
CC HSSP, P02901; IACP.
CC SMR, Q71YLO; 2-74.
CC TIGR, LMOF2365.1834; -.
CC HAMAP, MF_01217; -. 1.
CC InterPro, IPR009081; ACP_like.
CC InterPro, IPR003231; Acyl_carrier.
CC InterPro, IPR006163; Phosphopanteth_bd.
CC InterPro, IPR006162; Pantane_S.
CC Pfam, PF00550; PP-binding; 1.
CC ProDom, PD000887; Acyl_carrier; 1.
CC TIGRfam, TIGR00517; acyl_carrier; 1.
CC PROSITE, PS50075; ACP_DOMAIN; 1.
CC PROSITE, PS00012; PHOSPHOPANTHETHEINE; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
FT BINDING 37 37 Phosphopantetheine (covalent) (By
SQ SEQUENCE 77 AA; 8359 MW; 8DE7E28C1F192E21 CRC64;
similarity)
Query Match 71.5%; Score 284; DB 1; Length 77;
Best Local Similarity 80.8%; Pred. No. 1.1e-16;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 6 ADTERVTKIIVDRIGVDADYKLEASFKEDLGADSLDVLVLMLEDFEFMEISDEDAE 65
DB 2 AEVLEKVTIKIIVDRIGVEESKVTLEASFKEIDLGLADSLDVLVLMLEDFEFVEISDGDAE 61
QY 66 KIATVGDAVNYIO 78
DB 62 NINTVGDAVKYIIE 74

RESULT 14
ACP LISMO STANDARD; PRT; 77 AA.
AC P63439; Q92AK2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP)
GN Name=acpp; Synonyms=acpa; OrderedLocustNames=lmo1806;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_Taxid=1639;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=BGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangoul L., Buchrieser C., Ruhnlok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brant P., Chakraborty T.,
RA Charbit A., Chetouiari F., Couve E., de Narvar A., Denoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dusserget O.,
RA Entlan K.-D., Felli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maltournam A., Mata Vicente J., Ng B., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
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RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
RL Science 294:849-852(2001).
CC -1- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -1- PATHWAY: De novo fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL, AL591981; CAC99884.1; -, Genomic_DNA.
CC FIC, AF1300; AF1300.
CC HSSP, P80643; IHX8.
CC SMR, P63439; 2-74.
CC Listeria; LMO01806; -.
CC HAMAP, MF_01217; -. 1.
CC InterPro, IPR009081; ACP_like.
CC InterPro, IPR003231; Acyl_carrier.
CC InterPro, IPR006163; Phosphopanteth_bd.
CC InterPro, IPR006162; Pantane_S.
CC Pfam, PF00550; PP-binding; 1.
CC ProDom, PD000887; Acyl_carrier; 1.
CC TIGRfam, TIGR00517; acyl_carrier; 1.
CC PROSITE, PS50075; ACP_DOMAIN; 1.
CC PROSITE, PS00012; PHOSPHOPANTHETHEINE; 1.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
FT BINDING 37 37 Phosphopantetheine (covalent) (By
SQ SEQUENCE 77 AA; 8359 MW; 8DE7E28C1F192E21 CRC64;
similarity)
Query Match 71.5%; Score 284; DB 1; Length 77;
Best Local Similarity 80.8%; Pred. No. 1.1e-16;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 6 ADTERVTKIIVDRIGVDADYKLEASFKEDLGADSLDVLVLMLEDFEFMEISDEDAE 65
DB 2 AEVLEKVTIKIIVDRIGVEESKVTLEASFKEIDLGLADSLDVLVLMLEDFEFVEISDGDAE 61
QY 66 KIATVGDAVNYIO 78
DB 62 NINTVGDAVKYIIE 74

RESULT 15
ACP OCEIH STANDARD; PRT; 77 AA.
AC Q8ER06;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Acyl carrier protein (ACP).
GN Name=acpp; OrderedLocustNames=OB1525;
OS Oceanobacillus ihyenssis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_Taxid=182710;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=HT831 / DSM 14371 / JCM 11309;
RX MEDLINE=2220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA Takami H., Takaki Y., Uchiyama I.,
RT "Genome sequence of Oceanobacillus ihyenssis isolated from the Ihaya
RT Ridge and its unexpected adaptive capabilities to extreme
```



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RT environments."
RL Nucleic Acids Res. 30:3927-3935(2002).
CC -!- FUNCTION: Carrier of the growing fatty acid chain in fatty acid
CC biosynthesis (By similarity).
CC -!- PATHWAY: De novo fatty acid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC serine of apo-ACP by acps. This modification is essential for
CC activity because fatty acids are bound in thioester linkage to the
CC sulfhydryl of the prosthetic group (By similarity).
CC -!- SIMILARITY: Contains 1 acyl carrier domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000028; BAC13481.1; -; Genomic_DNA.
CC HSSP; P80643; 1F80.
CC SMR; OBER06; 2-76.
CC HAMAP; MF_01217; -; 1.
CC InterPro; IPR009081; ACP_like.
CC InterPro; IPR003231; Acyl_carrier.
CC InterPro; IPR006163; Phosphopanteth_bd.
CC InterPro; IPR006162; Pantane_S.
CC Pfam; PF00550; PP-binding; 1.
CC ProDom; PD000887; Acyl_carrier; 1.
CC TIGRfam; TIGR00517; acyl_carrier; 1.
CC PROSITE; PSS0075; ACP_DOMAIN; 1.
CC PROSITE; PSS0012; PHOSPHOPANTHEINE; FALSE_NEG.
CC Complete proteome; Fatty acid biosynthesis; Lipid synthesis;
CC Phosphopantetheine.
KW BINDING 37 phosphopantetheine (covalent) (By
FT similarity).
SQ SEQUENCE 77 AA; 8732 MW; E7BF70B5F7D4C77 CRC64;
Query Match 68.3%; Score 271; DB 1; Length 77;
Best Local Similarity 72.0%; Pred. No. 1.4e-15;
Matches 54; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
QY 6 ADTLERVTKIIVRLGVDAADVKELEASFKEDELGADSLDYVELVMELEDEFDEISDEDAE 65
DB 2 AEVFDVKEIITIDRLVRESKVTMEASFDDLDADSLDYVELVMELEDEFDEISDEDAE 61
QY 66 KIATVGDAVNYIQNQ 80
DB 62 KINTVGDAVDYINSK 76

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Search completed: December 21, 2005, 13:54:38
 Job time : 119.075 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:44 ; Search time 10.4776 Seconds
(without alignments)
743.830 Million cell updates/sec

Title: US-10-717-138-1

Sequence: 1 GPLSGADTLERVTIKIIVDR.....EDAEKATVGDANVTIONQ 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	370	93.2	77	JC4822	acyl carrier prote
2	313	78.8	77	B83961	acyl carrier prote
3	284	71.5	77	AF1300	acyl carrier prote
4	284	71.5	77	AF1672	acyl carrier prote
5	254	64.0	76	C64051	acyl carrier prote
6	244	61.5	77	T12052	acyl carrier prote
7	239	60.2	110	E82128	acyl carrier prote
8	236	59.4	77	F97115	acyl carrier prote
9	234	58.9	77	C89996	Hmb protein [impo
10	226.5	57.1	78	AC0195	acyl carrier prote
11	222	55.9	78	A70448	acyl carrier prote
12	220	55.4	78	T44435	acyl carrier prote
13	217.5	54.8	84	AG2223	acyl carrier prote
14	216	54.4	78	F81222	acyl carrier prote
15	215	54.2	78	AYEC	acyl carrier prote
16	215	54.2	78	AE0642	acyl carrier prote
17	215	54.2	78	D85672	acyl carrier prote
18	215	54.2	78	H90812	acyl carrier prote
19	213	53.7	78	A83276	acyl carrier prote
20	212	53.4	78	T12021	acyl carrier prote
21	212	53.4	78	A36778	acyl carrier prote
22	211	53.1	77	H71541	probable acyl carr
23	209	52.6	78	AG2711	acyl carrier prote
24	209	52.6	78	AE3436	acyl carrier prote
25	204	51.4	78	C87457	acyl carrier prote
26	203	51.1	77	D81695	acyl carrier prote
27	202	50.9	110	S77465	acyl carrier prote
28	202	50.9	110	F75333	acyl carrier prote
29	201	50.6	78	H71922	acyl carrier prote

30	200.5	50.5	79	2	D83411	probable acyl carr
31	200	50.4	77	2	G13838	acyl carrier prote
32	200	50.4	80	2	H84970	acyl carrier prote
33	197	49.6	79	2	G86527	acyl carrier prote
34	197	49.6	79	2	C72096	acyl carrier prote
35	196	49.4	81	2	C72349	acyl carrier prote
36	194	48.9	78	2	G64589	acyl carrier prote
37	193	48.6	80	2	S78295	acyl carrier prote
38	192.5	48.5	76	2	S13819	acyl carrier prote
39	192	48.4	80	2	A39452	acyl carrier prote
40	189	47.6	123	2	C71616	ACP XT0672 [impor
41	188	47.4	85	2	G82776	acyl carrier prote
42	187	47.1	84	2	S73201	acyl carrier prote
43	184.5	46.5	153	2	B64640	acyl carrier prote
44	184	46.3	69	2	B64728	acyl carrier prote
45	176	44.3	80	2	C41609	acyl carrier prote

ALIGNMENTS

RESULT 1
JC4822
acyl carrier protein - Bacillus subtilis
N:Alternate names: 8.5K protein
C:Species: Bacillus subtilis
C:Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4822; A69582
R:Oguro, A.; Kakeshita, H.; Takamatsu, H.; Nakamura, K.; Yamane, K.
Gene 172, 17-24, 1996
A:Title: The effect of Srb, a homologue of the mammalian SRP receptor alpha-subunit, on
A:Reference number: JC4819; MUID:96257247; PMID:8654983
A:Accession: JC4822
A:Molecule type: DNA
A:Residues: 1-77 <OGU>
A:Cross-references: UNIPROT:P80643; UNIPARC:UP10000603BF; DDBJ:D64116; NID:G1389548; PI
R:Kunzt, F.; Ogawara, N.; Mosser, I.; Albertin, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; Cho
A.; Enrich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogawara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Seto
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69582
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-77 <KON>
A:Cross-references: UNIPARC:UP10000603BF; GB:Z99112; GB:AL009126; NID:G2633902; PIDN:CT
A:Experimental source: strain 168
C:Genetics:
A:Gene: acpA; srb
C:Function:
A:Description: carrier of the growing fatty acid chain; growing fatty acid chain is cov
A:Pathway: fatty acid biosynthesis
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotei
F:2-73/Domain: acyl carrier protein homology <ACP>
F:37/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 93.2%; Score 370; DB 2; Length 77;
Best local similarity 100.0%; Pred. No. 4e-26;
Matches 76; Conservative 0; Indels 0; Gaps 0;

QY 6 ADTLERVTIKIIVDRLEGVDEADVLTLSFKEDLCADSLDVVELVMELEDFMEISDEDA 65

```
Db      2 ADLTERVTKIIVDRLGVDADVKLEASFKEDLGADSLDVVELVMELEDFEFGVEISDGDAAE 61
QY      66 KIATVGDAVNYIQNOQ 81
        |||||
Db      62 KIATVGDAVNYIQNOQ 77

RESULT 2
B83961
acyl-carrier protein acpA [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: B83961
R:Takami, H.; Nakaone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB3650; PMID:20512582; PMID:11058132
A:Accession: B83961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <STO>
A:Cross-references: UNIPROT:Q9KA04; UNIPARC:UPI0000125360; GB:AP001515; GB:BA000004; NID
A:Experimental source: strain C-125
C:Genetics:
A:Gene: acpA
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein

Query Match      78.8%; Score 313; DB 2; Length 77;
Best Local Similarity 81.6%; Pred. No. 4,2e-21;
Matches 62; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY      6 ADLTERVTKIIVDRLGVDADVKLEASFKEDLGADSLDVVELVMELEDFEFGVEISDGDAAE 65
        |||||
Db      2 ADLTSRITKIIVDRLGVDADVKLEASFKEDLGADSLDVVELVMELEDFEFGVEISDGDAAE 61

QY      66 KIATVGDAVNYIQNOQ 81
        |||||
Db      62 KIATVGDAVNYIEGRQ 77

RESULT 3
AF1300
acyl carrier proteins homolog acpA [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1300
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A>Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; PMID:21537279; PMID:11679669
A:Accession: AF1300
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <GLA>
A:Cross-references: UNIPROT:Q92AK2; UNIPARC:UPI0000555AC; GB:NC_003210; PIDN:CAC9884.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: acpA
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein

Query Match      71.5%; Score 284; DB 2; Length 77;
Best Local Similarity 80.8%; Pred. No. 1,5e-18;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY      6 ADLTERVTKIIVDRLGVDADVKLEASFKEDLGADSLDVVELVMELEDFEFGVEISDGDAAE 65
        |||||
        :|||
```

```
Db      2 AEVLEKVTKIIVDRLGVEESKVTLEASFKEDLGADSLDVVELVMELEDFEFGVEISDGDAAE 61
QY      66 KIATVGDAVNYIQ 78
        |||||
Db      62 NINTVGDAVKYIE 74

RESULT 4
AF1672
acyl carrier protein homolog acpA [imported] - Listeria innocua (strain C1p11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1672
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A>Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; PMID:21537279; PMID:11679669
A:Accession: AF1672
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <GLA>
A:Cross-references: UNIPROT:Q92AK2; UNIPARC:UPI0000555AC; GB:AL592022; PIDN:CAC97150.1;
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: acpA
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein

Query Match      71.5%; Score 284; DB 2; Length 77;
Best Local Similarity 80.8%; Pred. No. 1,5e-18;
Matches 59; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY      6 ADLTERVTKIIVDRLGVDADVKLEASFKEDLGADSLDVVELVMELEDFEFGVEISDGDAAE 65
        |||||
Db      2 AEVLEKVTKIIVDRLGVEESKVTLEASFKEDLGADSLDVVELVMELEDFEFGVEISDGDAAE 61

QY      66 KIATVGDAVNYIQ 78
        |||||
Db      62 NINTVGDAVKYIE 74

RESULT 5
CF4051
acyl carrier protein - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: CF4051
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: AF4000; PMID:95350630; PMID:7542800
A:Accession: CF4051
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-76 <TIG>
A:Cross-references: UNIPROT:P43709; UNIPARC:UPI0000125370; GB:U32701; GB:LA42023; NID:932
C:Genetics:
A:Gene: acpP
C:Function:
A:Description: carrier of the growing fatty acid chain; growing fatty acid chain is cova
A:Pathway: fatty acid biosynthesis
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotein
F11-72/Domain: acyl carrier protein homology <ACP>
F36/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
```


C:Genetics:
A:Gene: asx3342
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein

Query Match 54.8%; Score 217.5; DB 2; Length 84;
Best Local Similarity 58.2%; Pred. No. 1.2e-12;
Matches 46; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 3 LGSADTLERVTIIVDRIGVDEAD-VKLEASFKEKDGADSLDVVELVMELEDEPFMEISD 61
DB 1 MQSETFEKKVIVIEQLSVENPDVTPRASFANDQNSLDVVELVMALEEFPIEIPD 60

QY 62 EDAEKIATVGAADVNTIQN 80
DB 61 EAAEKITVQEAADVYNNQ 79

RESULT 14

F81222
acyl carrier protein NMB0220 [imported] - Neisseria meningitidis (strain MCS8 serogroup C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: F81222; E81995
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M. Science 287, 1809-1815, 2000

A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunloj, R.; Ve A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: F81222
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-78 <PRT>

A:Cross-references: UNIPROT:Q9UR72; UNIPARC:UPI0000125376; GB:AE002380; GB:AE002098; NID A:Experimental source: serogroup B, strain MCS8

R:Parhill, J.; Achman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: E81995

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-78 <PRT>

A:Cross-references: UNIPARC:UPI0000125376; GB:AL157959; NID:G7378778; PIDN: A:Experimental source: serogroup A, strain Z2491

C:Genetics:
A:Gene: acpP; NMB0220; NMA0043

C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein
F:2-73/Domain: acyl carrier protein homology <ACP>

Query Match 54.4%; Score 216; DB 2; Length 78;
Best Local Similarity 64.7%; Pred. No. 1.5e-12;
Matches 44; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 10 ERYTKIIVDLGVDEADVTLKASFKEDLGADSLDVVELVMELEDEPFMEISDPAKTIAT 69
DB 6 QQVKKIIVAEQLGVNEADVKNSSFPDDLGADSLDVVELVMALEBACCEIPDEDAKITT 65

QY 70 VGDVAVNYI 77
DB 66 VQALADYI 73

RESULT 15

AYEC
acyl carrier protein - Escherichia coli (strain K-12)

C:Species: Escherichia coli
C:Date: 24-Apr-1984 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: C42147; A92042; A26935; C64853; S28389; A03398

R:Rawlings, M.; Cronan Jr., J.E.
J. Biol. Chem. 267, 5751-5754, 1992

A:Title: The gene encoding Escherichia coli acyl carrier protein lies within a cluster o

A:Reference number: A42147; MUID:92210530; PMID:1556094

A:Accession: C42147

A:Molecule type: DNA

A:Residues: 1-78 <RAW>

A:Cross-references: UNIPROT:P02901; UNIPARC:UPI0000059F9B; GB:M84991; NID:G145879; PIDN: A:Experimental source: strain E-26

R:Vanaman, T.C.; Wakil, S.J.; Hill, R.L.
J. Biol. Chem. 243, 6420-6431, 1968

A:Title: The complete amino acid sequence of the acyl carrier protein of Escherichia col
A:Reference number: A92042; MUID:69063911; PMID:4882207

A:Accession: A92042

A:Molecule type: protein

A:Residues: 2-24, 'D', '26-78 <VAN>

A:Cross-references: UNIPARC:UPI000017469E
R:Vanaman, T.C.; Wakil, S.J.; Hill, R.L.

A:Title: The preparation of tryptic, peptic, thermolysin, and cyanogen bromide peptides
A:Reference number: A92041; MUID:69063910; PMID:4882206

A:Contents: annotation; partial sequence
J. Bacteriol. 169, 1469-1473, 1987

A:Reference number: A26935; MUID:87165751; PMID:3549687

A:Accession: A26935

A:Molecule type: protein

A:Residues: 2-43, 'I', '45-78 <JAC>

A:Cross-references: UNIPARC:UPI000017469F
A:Experimental source: strain K-12

R:Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co A:Title: The complete genome sequence of Escherichia coli K-12.
Science 277, 1453-1462, 1997

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: C64853

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-78 <BLAT>

A:Cross-references: UNIPARC:UPI0000059F9B; GB:AE000210; GB:U00096; NID:G1787332; PIDN:AA A:Experimental source: strain K-12, substrain MG1655

R:Niki, H.; Imanura, R.; Kikuchi, M.; Yamanaka, K.; Ogura, T.; Hiraga, S.
EMBO J. 11, 5101-5109, 1992

A:Title: E. coli MubB protein involved in chromosome partition forms a homodimer with a
A:Reference number: S28389; MUID:93099885; PMID:1464330

A:Accession: S28389

A:Molecule type: protein

A:Residues: 2-25, 'X', '27-35, 'XX', '38-41 <NIK>

A:Cross-references: UNIPARC:UPI00001746A0

C:Genetics:
A:Gene: acpP

A:Map position: 24 min
C:Function:

A:Description: carrier of the growing fatty acid chain; growing fatty acid chain is cov
A:Pathway: fatty acid biosynthesis
C:Superfamily: acyl/peptidyl carrier protein; acyl carrier protein homology
C:Keywords: carrier protein; fatty acid biosynthesis; phosphopantetheine; phosphoprotei
F:2-73/Domain: acyl carrier protein homology <ACP>
F:37/Binding site: phosphopantetheine (Ser) (covalent) #status experimental

Query Match 54.2%; Score 215; DB 1; Length 78;
Best Local Similarity 63.9%; Pred. No. 1.9e-12;
Matches 46; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

QY 10 ERYTKIIVDLGVDEADVTLKASFKEDLGADSLDVVELVMELEDEPFMEISDPAKTIAT 69
DB 6 ERYKTIIGQLGVKQGEVYNNASFVEDLGADSLDVVELVMALEBBERDTEIPBEAKITT 65

QY 70 VGDVAVNYIQN 81
DB 66 VQALADYINGHQ 77

Thu Dec 22 11:00:01 2005

us-10-717-138-1.rpr

Page 6

Search completed: December 21, 2005, 13:49:38
Job time : 10.4776 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 13:40:03 ; Search time 107.194 Seconds
(without alignments)
332.012 Million cell updates/sec

Title: US-10-717-138-1

Sequence: 1 GPLGSADTLERVTXIIIVRL.....EDAKIATVGAIVNTIQNOQ 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	100.0	81	5	AU10693 B. subtil
2	307	77.3	80	6	ABU18284 Protein e
3	284	71.5	77	6	ABBA9632 Listeria
4	284	71.5	77	6	ABU32958 Protein e
5	254	64.0	76	4	AU15380 Haemophil
6	254	64.0	76	6	ABU30165 Protein e
7	249	62.7	76	6	ABU39519 Protein e
8	239	60.2	110	6	ABU49449 Protein e
9	238	59.9	77	6	ABU43867 Protein e
10	238	59.9	77	6	ABU42995 Protein e
11	238	59.9	79	5	ABP39864
12	238	59.9	79	8	ADSO6306 Staphyloc
13	236	59.4	77	6	ABU23599 Protein e
14	234	58.9	77	4	AU137508 Staphyloc
15	234	58.9	77	4	AU137209 Staphyloc
16	234	58.9	77	4	AAEO2204 Staphyloc
17	234	58.9	77	6	ABU16490 Protein e
18	234	58.9	77	6	ABM73195 Staphyloc
19	234	58.9	77	9	ADW94686 Proteolitea
20	232	58.4	73	4	AU13966 Staphyloc
21	232	58.4	77	4	AU136531 Staphyloc
22	227	57.2	79	6	ABU23521 Protein e
23	226	57.1	78	6	ABU50649 Protein e
24	225	56.7	94	7	ADF07671 Bacterial

25	225	56.7	104	6	ABU24629	Abu24629 Protein e
26	223.5	56.3	48	5	AAW47181	Aam47181 Modular e
27	223.5	56.3	75	8	ADN25869	Adn25869 Bacterial
28	222.5	56.0	72	8	ADN24411	Adn24411 Bacterial
29	222.5	56.0	78	8	ADN21655	Adn21655 Bacterial
30	222.5	56.0	79	6	ABU19977	Abu19977 Protein e
31	222.5	56.0	79	6	ABU22402	Abu22402 Protein e
32	222.5	56.0	79	6	ABU21577	Abu21577 Protein e
33	222.5	56.0	80	9	ABM95361	Abm95361 M. xanthu
34	222	55.9	80	8	ADN17479	Adn17479 Bacterial
35	222	55.9	80	6	ADN10328	Adn10328 Allotococ
36	220	55.4	75	8	ADS42605	Ads42605 Bacterial
37	220	55.4	82	6	ABU33189	Abu33189 Protein e
38	220	55.4	82	9	AEBA1501	Aeba1501 L. pneumo
39	220	55.4	98	9	AEBA38214	Aeba38214 L. pneumo
40	217	54.7	71	8	ADN26458	Adn26458 Bacterial
41	217	54.7	76	8	ADS21595	Ads21595 Bacterial
42	217	54.7	78	6	ABP80257	Abp80257 N. gonorr
43	217	54.7	78	6	ABP78733	Abp78733 N. gonorr
44	217	54.7	78	6	ABU37226	Abu37226 Protein e
45	217	54.7	90	6	ABP78743	Abp78743 N. gonorr

ALIGNMENTS

RESULT 1
AU10693
ID AU10693 standard; protein; 81 AA.
XX
AC AU10693;
XX
DT 25-FEB-2002 (first entry)
XX
DE B. subtilis ACP used to grow ACP/ACPS complex crystals.
XX
KW Crystal structure; acyl carrier protein synthase; acyl carrier protein;
XX rational drug design method; antibiotic; 4'-phosphopantetheinyl; P-pant;
KW ACP/ACPS complex; protein co-ordinate data.
XX
XX Bacillus subtilis.
OS
XX
XX MO200185743-A2.
XX
XX 15-NOV-2001.
XX
XX 26-JAN-2001; 2001WO-US002949.
XX
XX 08-MAY-2000; 2000US-0202466P.
XX
XX (AMHP) AMERICAN HOME PROD CORP.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Pariss KD, Somers WS, Tam AS, Lin LL, Stahl ML, Powers R, Xu G;
XX WPI; 2002-055580/07.
XX
XX Crystallized complex useful in rational drug design methods, comprises
XX acyl carrier protein synthase and acyl carrier protein.
XX
XX Example 1; Fig 1; 147pp; English.
XX
XX The present invention relates to a crystallised structure comprising acyl
XX carrier protein synthase (ACPS) complexed with acyl carrier protein
XX (ACP). The invention also describes the solution structure of Bacillus
XX subtilis ACP. Both these structures are useful in rational drug design
XX methods for identifying agents that may interact with active sites of
XX ACPs and ACP, and for testing these agents to identify agents that may
XX represent novel antibiotics. They are also useful for design and
XX selection of potent and selective agents which interact with ACPs and
XX ACP, and for the design of antibiotics and other agents that interfere
XX with 4'-phosphopantetheinyl (P-pant) attachment, thus preventing
XX activation of corresponding carrier proteins. The present sequence

CC represents B. subtilis ACP used to grow ACP/ACPS complex crystals
XX SQ Sequence 81 AA;
Query Match 100.0%; Score 397; DB 5; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e-36;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GFLGSADTLERVTYKIYDRLGVDEADVLEASFKEDLGADSLDVVELVMELEDFEPMISD 60
DB 1 GFLGSADTLERVTYKIYDRLGVDEADVLEASFKEDLGADSLDVVELVMELEDFEPMISD 60
QY 61 DEDAEKATVGDVAVNYIQNQ 81
DB 61 DEDAEKATVGDVAVNYIQNQ 81
RESULT 2
ABU18284
ID ABU18284 standard; protein; 80 AA.
XX AC ABU18284;
XX DT 19-JUN-2003 (first entry)
XX OS Protein encoded by Prokaryotic essential gene #3811.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Bacillus anthracis.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JM;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX N-PSDB; ACA22154.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX DR Claim 25; SEQ ID NO 46208; 1766pp; English.
XX PS
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway of
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 80 AA;
Query Match 77.3%; Score 307; DB 6; Length 80;
Best Local Similarity 82.9%; Pred. No. 1.9e-26;
Matches 63; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 4 GSADTLERVTYKIYDRLGVDEADVLEASFKEDLGADSLDVVELVMELEDFEPMISD 63
DB 3 GMADVLERVTYKIYDRLGVDEETVVPASFKEDLGADSLDVVELVMELEDFEPMISD 62
QY 64 AEKATVGDVAVNYION 79
DB 63 AEKATVGDVAVNYIES 78
RESULT 3
ABB49632
ID ABB49632 standard; protein; 77 AA.
XX AC ABB49632;
XX DT 05-FEB-2002 (first entry)
XX OS Listeria monocytogenes protein #2336.
XX DE Listeria monocytogenes protein #2336.
XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX KW vitamin B12; bacterial infection; disease.
XX OS Listeria monocytogenes.
XX PN WO200177335-A2.
XX PD 18-OCT-2001.
XX PF 11-APR-2001; 2001WO-FR001118.
XX PR 11-APR-2000; 2000FR-00004629.
XX PA (INSP) INST PASTEUR.
XX PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Feihi H, Dehoux P;
XX PI Dusourget O, Chetouiati F, Nedjari H, Glaser P, Kunst F, Cossart P;
XX PI Daniels J, Goebel W, Kretz U, Kuhn W, Ng E, Vazquez-Boland JA;
XX PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
XX PI Charrabory T, Dommann E, Hain T, Berche P, Charbit A, Durant L;
XX PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
XX PI Madueno E, De Pablos B, Wehlend U, Kaerst U, Entian K, Hauf U;
XX PI Rose M, Voss H;
XX DR WPI; 2002-010914/01.
XX PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX PT and prevention of Listeria and related bacterial infections, and related
XX PT polypeptides.
XX PS Claim 6; SEQ ID NO 2337; 192pp; French.

PR	27-NOV-2000; 2000US-0253625P.	
PR	22-DEC-2000; 2000US-0257931P.	
PR	16-FEB-2001; 2001US-0269308P.	
XX	(ELIT-) ELITRA PHARM INC.	
XX		
PI	Haeelbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;	
PI	Yamamoto RT, Xu HH;	
XX	WPI; 2001-611495/70.	
DR	N-PSDB; AAS53239.	
XX		
PT	New polynucleotides for the identification and development of	
PT	antibiotics, comprise sequences of antisense nucleic acids.	
PS	Example 3; SEQ ID NO 10973; 511pp; English.	
XX		
CC	The invention relates to antisense inhibitors of genes essential to	
CC	prokaryotic cellular proliferation, their use in identifying the genes,	
CC	their use in the discovery of novel antibiotics, the essential genes,	
CC	themselves and the encoded proteins. The prokaryotes used are <i>Escherichia</i>	
CC	<i>coli</i> , <i>Staphylococcus aureus</i> , <i>Salmonella typhi</i> , <i>Klebsiella pneumoniae</i> ,	
CC	<i>Pseudomonas aeruginosa</i> and <i>Enterococcus faecalis</i> . The invention is also	
CC	useful for the identification of potential new targets for antibiotic	
CC	development. The antisense nucleic acids can also be used to identify	
CC	proteins used in proliferation, to express these proteins, and to obtain	
CC	antibodies capable of binding to the expressed proteins. The proteins can	
CC	be used to screen compounds in rational drug discovery programmes. The	
CC	antisense nucleic acid sequence is also useful to screen for homologous	
CC	nucleic acids which are required for cell proliferation in a wide variety	
CC	of organisms. The present sequence represents an essential prokaryotic	
CC	cellular proliferation protein. Note: The sequence data for this patent	
CC	did not form part of the printed specification, but was obtained in	
CC	electronic format directly from WPI at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SO	Sequence 76 AA;	
	Query Match 64.0%; Score 254; DB 4; Length 76;	
	Best Local Similarity 72.2%; Pred. No. 1.4e-20;	
	Matches 52; Conservative 8; Mismatches 12; Indels 0; Gaps 0;	
OY	10 ERVTKIYDRLGVDADYKLGASFKEEDLGADSLDVELVMELEDFEINSEDAEKIAT 69	
DB	5 ERVKKIIVYEQLGKVEDYKPEASFYEDIGADSLDVELVMALEBSFDIEIPDEAKIYT 64	
OY	70 VGDANYVYIQNOQ 81	
DB	65 VQSAIDVYQNNQ 76	
	RESULT 6	
ID	ABU30165 standard; protein; 76 AA.	
AC	ABU30165;	
XX		
DT	19-JUN-2003 (first entry)	
XX		
DE	Protein encoded by Prokaryotic essential gene #15692.	
XX		
KW	Antisense; prokaryotic essential gene; cell proliferation; drug design.	
XX		
OS	Haemophilus influenzae.	
XX		
PN	WO200277183-A2.	
XX		
PD	03-OCT-2002.	
PF	21-MAR-2002; 2002MO-US009107.	
XX		
XX	21-MAR-2001; 2001US-00815242.	
PR	06-SEP-2001; 2001US-00948993.	

[illegible]

DE Protein encoded by Prokaryotic essential gene #25046.
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XS
XN Pasteurella multocida.
PN WO200277183-A2.
PP 03-OCT-2002.
PD
PF 21-MAR-2002; 2002WO-US009107.
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
PX
PY (ELIT-) ELITRA PHARM INC.
PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PK WPI; 2003-029926/02.
PL N-PSDB; ACA43389.
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 67443; 1766bp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 76 AA:

Query Match 62.7%; Score 249; DB 6; Length 76;
Best Local Similarity 70.8%; Pred. No. 5.2e-20;
Matches 51; Conservative 9; Mismatches 12; Indels 0; Gaps 0

10 ERYVTKIIVRLGVDADVKLKASFKEDLGADSLDVVELVNELEDFPMESDSDAEKATAT 69
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
5 ERYVKTIIVDELGVKDEDVKEAFVFDLGDSDLDTVLVNLVAEEEPRIKIPDDEAKETTT 64
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

70 VGDAVNTIQQNQ 81
 65 VQSAIDVYQNNQ 76
 Db
 RESULT 8
 ID ABU49449
 ID ABU49449 standard; protein; 110 AA.
 AC ABU49449;
 XX
 DT 19-JUN-2003 (first entry)
 DE Protein encoded by Prokaryotic essential gene #34976.
 XX
 DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX KM
 XX OS Vibrio cholerae.
 OS
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002MO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 PA
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR MPI: 2003-029926/02.
 XX N-PSDB; ACAS319.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 77373; 1766bp; English.
 XX
 XX The invention relates to an isolated nucleic acid comprising any one of
 XX the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 110 AA;

Query Match 60.2%; Score 239; DB 6; Length 110;
Best Local Similarity 72.1%; Pred. No. 1,1e-18;
Matches 49; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 10 ERVTKIIVDRIGVDEADVLEASFKEDLGADSLDVLELMELDEDFMEISDEDAEKIAT 69
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 38 ERVKTIIVDRIGVDEADVLEASFKEDLGADSLDVLELMELDEDFMEISDEDAEKIAT 97
QY 70 VGDVAVNYI 77
|:|:|:
DB 98 VQAADIV 105

RESULT 9

ABU43867
ID ABU43867 standard; protein; 77 AA.

XX
AC ABU43867;

XX
DT 19-JUN-2003 (first entry)

XX
DE Protein encoded by Prokaryotic essential gene #29394.

XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
OS Staphylococcus haemolyticus.

XX
PN WO200277183-A2.

XX
PD 03-OCT-2002.

XX
PF 21-MAR-2002; 2002WO-US009107.

XX
PR 21-MAR-2001; 2001US-00815242.

XX
PR 06-SEP-2001; 2001US-00948993.

XX
PR 25-OCT-2001; 2001US-0342923P.

XX
PR 08-FEB-2002; 2002US-00072851.

XX
PR 06-MAR-2002; 2002US-0362699P.

XX
PA (ELIT-) ELITRA PHARM INC.

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
PI WPI; 2003-029926/02.

XX
DR N-PSDB; AKA47737.

XX
PS Claim 25; SEQ ID NO 71791; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 623 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the target of a compound that influences the cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 77 AA;

Query Match 59.9%; Score 238; DB 6; Length 77;
Best Local Similarity 67.1%; Pred. No. 8.8e-19;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 7 DTLSEVTKIIVDRIGVDEADVLEASFKEDLGADSLDVLELMELDEDFMEISDEDAEK 66
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 2 ENFDKVIIDVDRIGVADKXTEDASFKDDLGADSLDIAELVMELEDFMEISDEDAEK 61
QY 67 IATVGDVAVNYION 79
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 62 INTVGDVAVNYINS 74

RESULT 10

ABU42995
ID ABU42995 standard; protein; 77 AA.

XX
AC ABU42995;

XX
DT 19-JUN-2003 (first entry)

XX
DE Protein encoded by Prokaryotic essential gene #28522.

XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX
OS Staphylococcus epidermidis.

XX
PN WO200277183-A2.

XX
PD 03-OCT-2002.

XX
PF 21-MAR-2002; 2002WO-US009107.

XX
PR 21-MAR-2001; 2001US-00815242.

XX
PR 06-SEP-2001; 2001US-00948993.

XX
PR 25-OCT-2001; 2001US-0342923P.

XX
PR 08-FEB-2002; 2002US-00072851.

XX
PR 06-MAR-2002; 2002US-0362699P.

XX
PA (ELIT-) ELITRA PHARM INC.

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX
PI WPI; 2003-029926/02.

XX
DR N-PSDB; AKA46865.

XX
PS Claim 25; SEQ ID NO 70919; 1766pp; English.

XX New antisense nucleic acids, useful for identifying proteins or screening
CC for homologous nucleic acids required for cellular proliferation to
CC isolate candidate molecules for rational drug discovery programs.

PT treating an *S. epidermidis* bacterial infection.
XX
PS Claim 17; SEQ ID NO 5601; 741pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a nucleotide
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
CC 1-3772) and encoding an *Staphylococcus epidermidis* polypeptide with any
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
CC given in the specification. Also described are: a recombinant expression
CC vector; a cell comprising a recombinant expression vector of (1);
CC producing an *S. epidermidis* polypeptide; an isolated nucleic acid
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
CC vaccine composition for prevention or treatment of an *S. epidermidis*
CC infection, comprising a nucleic acid cited above and a carrier; treating
CC a subject for *S. epidermidis* infection; a recombinant or substantially
CC pure preparation of an *S. epidermidis* polypeptide or its fragment; a
CC vaccine composition for prevention or treatment of an *S. epidermidis*
CC infection; detecting the presence of a *Staphylococcus* nucleic acid in a
CC sample; a computer readable medium having recorded in it the nucleotide
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
CC system for identifying fragments of the *Staphylococcus* genome of
CC commercial importance; a computer based system for identifying fragments
CC of the *Staphylococcus* plasmids of commercial importance; identifying
CC commercially important nucleic acid fragments of the *Staphylococcus*
CC genome and/or plasmids; and identifying an expression modulating fragment
CC of the *Staphylococcus* genome and/or plasmids. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of an *Staphylococcus epidermidis* bacterial
CC infection. This is the amino acid sequence of a *S. epidermis* protein of
CC the invention.
XX
SQ Sequence 79 AA:
XX
SQ
XX
Query Match 59.9%; Score 238; DB 8; Length 79;
Best Local Similarity 67.1%; Pred. No. 9.1e-19;
Matches 49; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
XX
QY 7 DTLERTKIIVRLGADVLTLEASFKEDLGADSLVVELVMELEDFDMEISPDAAK 66
DB 4 EHFDPKVDIIVRLGADVLTLEASFKEDLGADSLVVELVMELEDFDMEISPDAAK 63
XX
QY 67 IATVGDVAVNYION 79
DB 64 INTVGDVAVKINS 76
XX
RESULT 13
ABU23599
ID ABU23599 standard; protein; 77 AA.
XX
AC ABU23599;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #9126.
XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS *Clostridium acetobutylicum*.
XX
PN WO20027183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
XX
PR 06-SEP-2001; 2001US-00948993.
XX
PR 25-OCT-2001; 2001US-0342823P.
XX
PR 08-FEB-2002; 2002US-00072851.
XX
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.

XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
XX
DR N-PSDB; ACA27469.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 51523; 1766pp; English.
XX
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC the gene product or that has an activity against a biological pathway
CC of the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ
XX
SQ Sequence 77 AA:
XX
XX
Query Match 59.4%; Score 236; DB 6; Length 77;
Best Local Similarity 60.9%; Pred. No. 1.5e-18;
Matches 42; Conservative 18; Mismatches 9; Indels 0; Gaps 0;
XX
QY 10 ERYTKIIVRLGADVLTLEASFKEDLGADSLVVELVMELEDFDMEISPDAAKAT 69
DB 4 EKVYDIADQIGIDATETKIMSSFTDDGADSLVVELVMELEDFDMEISPDAAKAT 63
XX
QY 70 VGDVAVNYIQ 78
DB 64 VGDVAVNYIK 72
XX
RESULT 14
AAU37508
ID AAU37508 standard; protein; 77 AA.
XX
AC AAU37508;
XX
DT 14-FEB-2002 (first entry)
XX
DE *Staphylococcus aureus* cellular proliferation protein #1678.
XX
KM Antisense; prokaryotic cellular proliferation protein; antibiotic;
XX
KW antibacterial; drug design.
XX

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